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(54) Title: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE PROTEINS OF THERAPEUTIC POTENTIAL

(57) Abstract: A computational method for identifying adhesin and adhesin-like proteins, said method comprising steps of computing the sequence-based attributes of a neural network software wherein the attributes are (i) amino acid frequencies, (ii) multiplet frequency, (iii) dipeptide frequencies, (iv) charge composition, and (v) hydrophobic composition, training the artificial neural Network (ANN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins having probability of being an adhesin (P_{ad}) as ≥ 0.51; a computer system for performing the method; and genes and proteins encoding adhesin and adhesin-like proteins.

COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE PROTEINS OF THERAPEUTIC POTENTIAL

Field of the present Invention

A computational method for identifying adhesin and adhesin-like proteins; computer system for performing the method; and genes and proteins encoding adhesin and adhesin-like proteins

Background and prior art of the present Invention

The progress in genome sequencing projects has generated a large number of inferred protein sequences from different organisms. It is expected that the availability of the information on the complete set of proteins from infectious human pathogens will enable us to develop novel molecular approaches to combat them. A necessary step in the successful colonization and subsequent manifestation of disease by microbial pathogens is the ability to adhere to host cells.

Microbial pathogens encode several proteins known as adhesins that mediate their adherence to host cell surface receptors, membranes, or extracellular matrix for successful colonization. Investigations in this primary event of host-pathogen interaction over the past decades have revealed a wide array of adhesins in a variety of pathogenic microbes. Presently, substantial information on the biogenesis of adhesins and the regulation of adhesin factors is available. One of the best understood mechanisms of bacterial adherence is attachment mediated by pili or fimbriae. Several afimbrial adhesins also have been reported. In addition, limited knowledge on the target host receptors also has been gained (Finlay, B.B. and Falkow, S 1997).

New approaches to vaccine development focus on targeting adhesins to abrogate the colonization process (Wizemann, *et al* 1999). However, the specific role of particular adhesins has been difficult to elucidate. Thus, prediction of adhesins or adhesin-like proteins and their functional characterization is likely to aid not only in deciphering the molecular mechanisms of host pathogen interaction but also in developing new vaccine formulations, which can be tested in suitable experimental model systems.

One of the best understood mechanisms of bacterial adherence is attachment mediated by pili or fimbriae. For example, FimH and PapG adhesins of *Escherichia coli* (Maurer, L., Orndorff, P.(1987), Bock, K., *et al.*(1985). Other examples of pili group adhesins include type IV pili in *Pseudomonas aeruginosa*, Neisseria species, Moraxella species, Enteropathogenic *Escherichia coli* and *Vibrio cholerae* (Sperandio V *et al* (1996).

Several afimbrial adhesins are HMW proteins of *Haemophilus influenzae* (van Schilfgaarde 2000), the filamentous hemagglutinin, pertactin, of *Bordetella pertussis* (Bassinet *et al* 2000), the BabA of *H. pylori* (Yu J *et al* 2002) and the YadA adhesin of *Yersinia enterocolitica* (Neubauer *et al* 2000). The intimin receptor protein (Tir) of Enteropathogenic *E. coli* (EPEC) is another type of adhesin (Ide T *et al* 2003). Other class of adhesins includes MrkD protein of *Kleibsella pneumoniae*, Hia of *H. influenzae* (St Geme *et al* 2000), Ag I/II of *Streptococcus mutans* and SspA, SspB of *Streptococcus gordonii* (Egland *et al* 2001), FnbA, FnbB of *Staphylococcus aureus* and SfbI, protein F of *Streptococcus pyogenes* , the PsaA of *Streptococcus pneumoniae* (De *et al* 2003).

A known example of adhesins approved as vaccine is the acellular pertussis vaccine containing FHA and pertactin against *B. pertussis* the causative agent of whooping cough (Halperin, S *et al* 2003). Immunization with FimH is being evaluated for protective immunity against pathogenic *E. coli* (Langermann S *et al* 2000), in *Streptococcus pneumoniae*, PsaA is being investigated as a potential vaccine candidate against pneumococcal disease (Rapola, S *et al* 2003). Immunization results with BabA adhesin showed promise for developing a vaccine against *H. pylori* (Prinz, C *et al* 2003). A synthetic peptide sequence anti-adhesin vaccine is being evaluated for protection against *Pseudomonas aeruginosa* infections.

Screening for adhesin and adhesin like proteins by conventional experimental method is laborious, time consuming and expensive. As an alternative, homology search is used to facilitate the identification of adhesins. Although, this procedure is useful in the analysis of genome organization (Wolf *et al* 2001) and of metabolic pathways (Peregrin-Alvarez *et al* 2003, Rison *et al* 2002), it is somewhat limited in allowing functional predictions when the homologues are not functionally characterized or the sequence divergence is high. Assignment of functional roles to proteins based on this technique has been possible for only about 60% of the predicted protein sequences (Fraser *et al* 2000). Thus, we explored the possibility of developing a non-homology method based on sequence composition properties combined with the power of the Artificial Neural Networks to identify adhesins and adhesin-like proteins in species belonging to wide phylogenetic spectrum.

Twenty years ago, Nishikawa *et al* carried out some of the early attempts to classify proteins into different groups based on compositional analysis (Nishikawa *et al* 1983).

More recently, the software PropSearch was developed for analyzing protein sequences where conventional alignment tools fail to identify significantly similar sequences (Hobohm, U. and Sander, C 1995). PropSearch uses 144 compositional properties of protein sequences to detect possible structural or functional relationships between a new sequence and sequences in the database. Recently the compositional attributes of proteins have been used to develop softwares for predicting secretory proteins in bacteria and apicoplast targeted proteins in *Plasmodium falciparum* by training Artificial Neural Networks (Zuegge *et al* 2001).

Zuegge et al have used the 20 amino acid compositional properties. Their objective was to extract features of apicoplast targeted proteins in *Plasmodium falciparum*. This is distinct from our software SPAAN that focuses on adhesins and adhesin-like proteins involved in host-pathogen interaction.

Hobohm and Sander have used 144 compositional properties including isoelectric point and amino acid and dipeptide composition to generate hypotheses on putative functional role of proteins that are refractory to analysis using other sequence alignment based approaches like BLAST and FASTA. Hobohm and Sander do not specifically address the issue of adhesins and adhesin-like proteins, which is the focus of SPAAN

Nishikawa et al had originally attempted to classify proteins into various functional groups. This was a curiosity driven exercise but eventually lead to the development of a software to discriminate extra-cellular proteins from intracellular proteins. This work did not address the issue of adhesins and adhesin-like proteins, which is the focus of SPAAN.

Thus, none of the aforementioned research groups have been able to envisage the methodology of the instant application. The inventive method of this application provides novel proteins and corresponding gene sequences.

Adhesins and adhesin-like proteins mediate host-pathogen interactions. This is the first step in colonization of a host by microbial pathogens. Attempts Worldwide are focused on designing vaccine formulations comprising adhesin proteins derived from pathogens. When immunized, host will have its immune system primed against adhesins for that pathogen. When a pathogen is actually encountered, the surveillance mechanism will recognize these adhesins, bind them through antigen-antibody interactions and neutralize the pathogen through complement mediate cascade and other related clearance mechanisms. This strategy has been successfully employed in

the case of Whooping cough and is being actively pursued in the case of Pneumonia, Gastric Ulcer and Urinary tract infections.

Objects of the present Invention

The main object of the present invention is to provide a computational method for identifying adhesin and adhesin-like proteins of therapeutic potential.

Another object of invention is to provide a method for screening the proteins with unique compositional characteristics as putative adhesins in different pathogens.

Yet, another object of the invention is providing the use of gene sequences encoding the putative adhesin proteins useful as preventive therapeutics.

Summary of the present Invention

A computational method for identifying adhesin and adhesin-like proteins, said method comprising steps of computing the sequence-based attributes of protein sequences using five attribute modules of software SPAAN, (i) amino acid frequencies, (ii) multiplet frequency, (iii) dipeptide frequencies, (iv) charge composition, and (v) hydrophobic composition, training the artificial neural Network (ANN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins having probability of being an adhesin (P_{ad}) as ≥ 0.51; a computer system for performing the method; and genes and proteins encoding adhesin and adhesin-like proteins

Detailed description of the present Invention

Accordingly, the present invention relates to a computational method for identifying adhesin and adhesin-like proteins, said method comprising steps of computing the sequence-based attributes of protein sequences using five attribute modules of software SPAAN, (i) amino acid frequencies, (ii) multiplet frequency, (iii) dipeptide frequencies, (iv) charge composition, and (v) hydrophobic composition, training the artificial neural Network (ANN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins having probability of being an adhesin (P_{ad}) as ≥ 0.51; a computer system for performing the method; and genes and proteins encoding adhesin and adhesin-like proteins

In an embodiment of the present invention, wherein the invention relates to a computational method for identifying adhesin and adhesin-like proteins, said method comprising steps of:

a. computing the sequence-based attributes of protein sequences using five attribute modules of a neural network software, wherein the attributes

are software, (i) amino acid frequencies, (ii) multiplet frequency, (iii) dipeptide frequencies, (iv) charge composition, and (v) hydrophobic composition,

b. training the artificial neural Network (ANN) for each of the computed five attributes, and

c. identifying the adhesin and adhesin-like proteins having probability of being an adhesin (P_{ad}) as ≥ 0.51.

In another embodiment of the present invention, wherein the invention relates to a method wherein the protein sequences is obtained from pathogens, eukaryotes, and multicellular organisms.

In an embodiment of the present invention, wherein the invention relates to a method, wherein the protein sequences are obtained from the pathogens selected from a group of organisms comprising *Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Mycoplasma pneumoniae, Mycobacterium tuberculosis, Rickettsiae prowazekii, Porphyromonas gingivalis, Shigella flexneri, Streptococcus mutans, Streptococcus pneumoniae, Neisseria meningitides, Streptococcus pyogenes, Treponema pallidum* and Severe Acute Respiratory Syndrome associated human coronavirus (SARS).

In yet another embodiment of the present invention, wherein the method of the invention is a non-homology method.

In still another embodiment of the present invention, wherein the invention relates to the method using 105 compositional properties of the sequences.

In still another embodiment of the present invention, wherein the invention relates to a method showing sensitivity of at least 90%.

In still another embodiment of the present invention, wherein the invention relates to the method showing specificity of 100%.

In still another embodiment of the present invention, wherein the invention relates to a method identifying adhesins from distantly related organisms.

In still another embodiment of the present invention, wherein the invention relates to the neural network has multi-layer feed forward topology, consisting of an input layer, one hidden layer, and an output layer.

In still another embodiment of the present invention, wherein the invention relates to the number of neurons in the input layer are equal to the number of input data points for each attribute.

In still another embodiment of the present invention, wherein the invention relates to the "P_{ad}" is a weighted linear sum of the probabilities from five computed attributes.

In still another embodiment of the present invention, wherein the invention relates to each trained network assigns a probability value of being an adhesin for the protein sequence.

In still another embodiment of the present invention, wherein the invention relates to a computer system for performing the method of claim 1, said system comprising a central processing unit, executing SPAAN program, giving probabilities based on different attributes using Artificial Neural Network and in built other programs of assessing attributes, all stored in a memory device accessed by CPU, a display on which the central processing unit displays the screens of the above mentioned programs in response to user inputs; and a user interface device.

In still another embodiment of the present invention, wherein the invention relates to a set of 274 annotated genes encoding adhesin and adhesin-like proteins, having SEQ ID Nos. 385 to 658.

In still another embodiment of the present invention, wherein the invention relates to a set of 105 hypothetical genes encoding adhesin and adhesin-like proteins, having SEQ ID Nos. 659 to 763.

In still another embodiment of the present invention, wherein the invention relates to a set of 279 annotated adhesin and adhesin-like proteins of SEQ ID Nos. 1 to 279.

In still another embodiment of the present invention, wherein the invention relates to a set of 105 hypothetical adhesin and adhesin-like proteins of SEQ ID Nos. 280 to 384.

One more embodiment of the present invention, wherein the invention also relates to a fully connected multilayer feed forward Artificial Neural Network based on the computational method as claimed in claim 1, comprising of an input layer, a hidden layer and an output layer which are connected in the said sequence, wherein each neuron is a binary digit number and is connected to each neuron of the subsequent layer for identifying adhesin or adhesin like proteins, wherein the program steps comprise:-

[a] feeding a protein sequence in FASTA format; [b] processing the sequence obtained in step [a] through the 5 modules named A, C, D, H and M, wherein attribute A represents an amino acid composition, attribute C represents a charge composition, attribute D represents a dipeptide composition of the 20 dipeptides [NG, RE, TN, NT, GT, TT, DE, ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI and HR], attribute H

represents a hydrophobic composition and attribute M represents amino acid frequencies in multiplets to quantify 5 types of compositional attributes of the said protein sequence to obtain numerical input vectors respectively for each of the said attributes wherein the sum of numerical input vectors is 105; [c] processing of the numerical input vectors obtained in step [b] by the input neuron layer to obtain signals, wherein the number of neurons is equal to the number of numerical input vectors for each attribute; [d] processing of signals obtained from step [c] by the hidden layer to obtain synaptic weighted signals, wherein the optimal number of neurons in the hidden layer was determined through experimentation for minimizing the error at the best epoch for each network individually; [e] delivering synaptic weighted signals obtained from step [d] to the output layer for assigning of a probability value for each protein sequence fed in step [a] as being an adhesin by each network module; [f] using the individual probabilities obtained from step [e] for computing the final probability of a protein sequence being an adhesin denoted by the P_{ad} value, which is a weighted average of the individual probabilities obtained from step [e] and the associated fraction of correlation which is a measure of the strength of the prediction.

In still another embodiment of the present invention, wherein the input neuron layer consists of a total of 105 neurons corresponding to 105 compositional properties.

In still another embodiment of the present invention, wherein the hidden layer comprises of neurons represented as 30 for amino acid frequencies, 28 for multiplet frequencies, 28 for dipeptide frequencies, 30 for charge composition and 30 for hydrophobic composition.

In still another embodiment of the present invention, wherein the output layer comprises of neurons to deliver the output values as probability value for each protein sequence.

Identification of novel adhesins and their characterization are important for studying host-pathogen interactions and testing new vaccine formulations. We have employed Artificial Neural Networks to develop an algorithm SPAAN (Software for Prediction of Adhesin and Adhesin-like proteins using Neural Networks) that can identify adhesin proteins using 105 compositional properties of a protein sequence. SPAAN could correctly predict well characterized adhesins from several bacterial species and strains. SPAAN showed 89% sensitivity and 100% specificity in a test data set that did not

contain proteins in the training set. Putative adhesins identified by the software can serve as potential preventive therapeutics.

The present invention provides a novel computational method for identifying adhesin and adhesin-like proteins of therapeutic potential. More particularly, the present invention relates to candidate genes for these adhesins. The invention further provides new leads for development of candidate genes, and their encoded proteins in their functional relevance to preventive approaches. This computational method involves calculation of several sequence attributes and their subsequent analyses lead to the identification of adhesin proteins in different pathogens. Thus, the present invention is useful for identification of the adhesin proteins in pathogenic organisms. The adhesin proteins from different genomes constitute a set of candidates for functional characterization through targeted gene disruption, microarrays and proteomics. Further, these proteins constitute a set of candidates for further testing in development of preventive therapeutics. Also, are provided the genes encoding the candidate adhesin proteins.

The present method offers novelty in the principles used and the power of Neural Networks to identify new adhesins compared to laborious and time consuming conventional methods. The present method is based on compositional properties of proteins instead of sequence alignments. Therefore this method has the ability to identify adhesin and adhesin like proteins from bacteria belonging to a wide phylogenetic spectrum. The predictions made from this method are readily verifiable through independent analysis and experimentation. The invention has the potential to accelerate the development of new preventive therapeutics, which currently requires high investment in terms of requirement of skilled labor and valuable time.

The present invention relates to a computational method for the identification of candidate adhesin proteins of therapeutic potential. The invention particularly describes a novel method to identify adhesin proteins in different genomes of pathogens. These adhesin proteins can be used for developing preventive therapeutics.

Accordingly, a computational method for identifying adhesin and adhesin-like proteins of therapeutic potential which comprises calculation of 105 compositional properties under the five sequence attributes, namely, Amino Acid frequency, Multiplet frequency, dipeptide frequency, charge composition and hydrophobic composition; and then training Artificial Neural Network (ANN, Feed Forward Error Back Propagation)

using these properties for differentiating between adhesin and non-adhesin class of proteins. This computational method involves quantifying 105 compositional attributes of query proteins and qualifying them as adhesins or non-adhesins by a P_{ad} value (Probability of being an adhesin). The present invention is useful for identification of adhesin and adhesin-like proteins in pathogenic organisms. These newly identified adhesin and adhesin-like proteins constitute a set of candidates for development of new preventive therapeutics that can be tested in suitable experimental model systems readily. In addition, the genes encoding the candidate adhesin and adhesin-like proteins are provided.

The invention provides a set of candidate adhesin and adhesin-like proteins and their coding genes for further evaluation as preventive therapeutics. The method of invention is based on the analysis of protein sequence attributes instead of sequence patterns classified to functional domains. Present method is less dependent on sequence relationships and therefore offers the potential power of identifying adhesins from distantly related organisms. The invention provides a computational method, which involves prediction of adhesin and adhesin-like proteins using Artificial Neural Networks. The proteins termed adhesin were found to be predicted with a high probability (P_{ad} 0.51) in various pathogens. Some adhesin sequences turned out to be identical or homologous to proteins that are antigenic or implicated in virulence. By this approach, proteins could be identified and short-listed for further testing in development of new vaccine formulations to eliminate diseases caused by various pathogenic organisms.

DESCRIPTION OF TABLES

Table 1: Output file format given by SPAAN.

Table 2: Organism Name, Accession number, Number of base pairs, Date of release and Total number of proteins.

Table 3. Prediction of well characterized adhesins from various bacterial pathogens using SPAAN.

Table 4. Analysis of predictions made by SPAAN on genome scans of a few selected pathogenic organisms.

Table 5: GI numbers and Gene IDs of new putative adhesins predicted by SPAAN in the genomes listed in Table 2.

Table 6: GI numbers and Gene IDs of hypothetical proteins predicted as putative adhesins by SPAAN in the genomes listed in Table 2.

Table 7: The list of 198 adhesins found in bacteria

Brief description of the accompanying drawings

Figure 1 shows the Neural Network architecture

Figure 2 shows assessment of SPAAN using defined test dataset.

Figure 3 (a) shows Histogram plots of the number of proteins in the various P_{ad} value ranges are shown. **(b)** Pairwise sequence relationships among the adhesins were determined using CLUSTAL W and plotted on X-axis. Higher scores indicate similar pairs. **(c)** plot for non-adhesins. Data are plotted in the 4 quadrant format for clear inspection.

Software program was written in C Language and operated on Red Hat Linux 8.0 operating system. The computer program accepts input protein sequences in FastA format and produces a tabulated output. The output Table contains one row for each protein listing the probability outputs of each of the five modules, a weighted average probability of these five modules (P_{ad}), and the function of the protein as described in the input sequence file. This software is called SPAAN (A Software for Prediction of Adhesins and Adhesin-like proteins using Neural Networks) and a software copyright has been filed. Although this software has multiple modules, the running of these modules have been integrated and automated. The user only needs to run one command.

AAcompo.c:

Input: File containing protein sequences in the fasta format.

Output: File containing frequencies of all 20 AAs for each protein in one row.

charge.c:

Input: File containing protein sequences in the fasta format.

Output: File containing frequency of charged amino acids (R, K, E and D) and moments (up to 18th order) of the positions of charged amino acids.

hdr.c:

Input: File containing protein sequences in the fasta format.

Output: File containing frequencies of 5 groups of amino acids formed on the basis their Hydrophobicity and moments of their positions up to 5th order.

multiplets.c:

Input: File containing protein sequences in the fasta format.
Output: File containing fractions of multiplets of each of the 20 amino acids.

querydipep.c:

Input: File.1 containing protein sequences in the fasta format.
File.2 containing list of the significant dipeptides in dipeptide analysis.
Output: File containing frequencies of the dipeptides listed in the input File.2 for each protein in the input File.1.

train.c:

Input: File containing following specifications –

1. Number of input and output parameters.
2. Number of nodes in the hidden layers.
3. Names of the training, validate and test data files.
4. Learning rate, coefficient of moment.
5. Maximum number of cycles for training.

Output: Outputs are as follows.

1. Output of the trained NN for the test data set.
2. Values of the weight connections in the trained NN.
3. Some extra information about training.

recognize.c:

Input: File containing following specifications –

1. Number of input and output parameters.
2. Number of nodes in the hidden layers.
3. Names of the query input file.
4. Name of the file containing values of the weight connections for trained NN.
5. Name of the output file.

Output: Outputs for the query entries calculated by the trained NN.

standard.c:

Input: File containing protein sequences in fasta format.

Output: File containing protein sequences in fasta format with all the new line characters removed lying within a sequence.

filter.c:

Input: File containing protein sequences in fasta format.

Output: File containing protein sequences from the input except those which are short in length (<50 AAs) and which contain any amino acid other than the 20 known amino acids.

The five attributes:

Amino Acid frequencies

Amino acid frequency f_i = (counts of ith amino acid in the sequence) / l ; i, = 1...20, l is the length of the protein.

Multiplet frequency

Multiplets are defined as homopolymeric stretches $(X)_n$ where X is any of the 20 amino acids and n is an integer > 2. After identifying all the multiplets, the frequencies of the amino acids in the multiplets were computed as

$f_i(m)$ = (counts of i^{th} amino acid occurring as multiplet) / l

Dipeptide frequencies

The frequency of a dipeptide (i, j) f_{ij} = (counts of ij^{th} dipeptide) / (total dipeptide counts); i, j ranges from 1 to 20.

It has been found that dipeptide repeats in proteins are important for functional expression of the clumping factor present on *Staphylococcus aureus* cell surface that binds to fibrinogen (Hartford *et al* 1999). Thus we included the dipeptide frequency module. The total number of dipeptides is 400. For optimal training of Neural Network, the ratio of total number of input vectors to the total number of weight connections must be around 2 to avoid over fitting (Andrea *et al*). Therefore, we identified the dipeptides whose frequencies in the adhesin data set (469 proteins, see database construction) were significantly different from that in the non-adhesin dataset (703 proteins) using *t-test*. The frequencies of top 20 dipeptides (when arranged in the descending order of the p-values of *t-test*), were fed to the Neural Network. These dipeptides were (using single letter IUPAC-IUB code) NG, RE, TN, NT, GT, TT, DE,

ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI, AND HR. With frequency inputs for 20 dipeptides and 28 neurons in the 2nd layer, the total number of weight connections is 588, and is in keeping with the criterion of avoiding over fitting.

Charge composition

The input frequency of charged amino acids (R, K, E and D considering the ionization properties of the side chains at pH 7.2) given by f_c = (counts of charged amino acids) / l Further, information on the characteristics of the distribution of the charged amino acids in a given protein sequence was provided by computing the moments of the positions of the occurrences of the charged amino acids. Since moments characterize the patterns of distribution such as skewness and kurtosis (sharpness of the peak) we have used them to represent the distribution patterns of the charged residues in the sequence.

The general expression to compute moments of a given order; say 'i' is

$M_r = r^{th}$ order moment of the positions of charged amino acids

$$= \sum \frac{(X_i - X_m)^r}{N}$$

Where, X_m = mean of all positions of charged amino acids

X_i = position of i^{th} charged amino acid

N = number of charged amino acids in the sequence

The moments 2^{nd} to 19^{th} order were used to train the ANN constituting a total 20 inputs in addition to frequency of charged amino acids and the length of the protein. The upper limit of 19^{th} order was set based on assessments of sensitivity and specificity on a small dataset of adhesins and non-adhesins. Moments of order greater than 19 were not useful in improvement of performance.

Hydrophobic composition

A given protein sequence was digitally transformed using the hydrophobic scores of the amino acids according to Brendel *et al.* (43). The scores for five groups of amino acids: (-8 for K, E, D, R), (-4 for S, T, N, Q), (-2 for P, H), (+1 for A, G, Y, C, W), (+2 for L, V, I, F, M).

Following inputs were given for each of the group

(a) f_i = (counts of i^{th} group) / (total counts in the protein); i ranges from 1 to 5

(b) $m_{ji} = j^{th}$ order moment of positions of amino acids in i^{th} group; j ranges from 2 to 5.

A total of 25 inputs representing the hydrophobic composition of a protein were fed to the Neural Network. The rationale for using moments was same as described in the section on charge composition inputs.

Taken together a total of 105 compositional properties of a given protein sequence were used to predict their adhesin characteristics.

The software PropSearch uses 144 compositional properties of protein sequences to detect possible structural or functional relationships between a new sequence and sequences in the database (Hobohm and Sander 1995). The approach defines protein sequence dissimilarity (or distance) as a weighted sum of differences of compositional properties such as singlet and doublet amino acid composition, molecular weight, isoelectric point (protein property search or PropSearch). Compositional properties of proteins have also been used for predicting secretory proteins in bacteria and apicoplast targeted proteins in Plasmodium falciparum (Zuegge, et al. 2001). The properties used here are statistical methods, principal component analysis, self-organizing maps, and supervised neural networks. In SPAAN, we have used 105 compositional properties in the five modules viz. Amino Acid frequencies, Multiplet frequencies, Dipeptide frequencies, Charge composition, Hydrophobic composition. The total of 105 properties used in SPAAN are 20 for Amino acid frequencies, 20 for Multiplets frequencies, 20 for Dipeptide frequencies (Top 20 significant dipeptides are used, based on *t-test*), 20 for Charge composition (frequency of charged amino acids (R, K, E and D) and moments of 2nd to 19th order), and 25 for Hydrophobic composition (Amino acids were classified into five groups (-8 for K, E, D, R), (-4 for S, T, N, Q), (-2 for P, H), (+1 for A, G, Y, C, W), (+2 for L, V, I, F, M). A total of 25 inputs consisted of the following: Frequency of each group, Moments of positions of amino acids in each group from 2nd to 5th order.

Neural Network

A feed forward error back propagation Neural Network was used. The program is a kind gift from Charles W. Anderson, Department of Computer Science, Colorado State University, Fort Collins, CO 80523, anderson@cs.colostate.edu

Neural Network architecture

The Neural Network used here has a multi-layer feed-forward topology. It consists of an input layer, one hidden layer and an output layer. This is a 'fully-connected' Neural Network where each neuron i is connected to each unit j of the next layer (Figure 1).

The weight of each connection is denoted by w_{ij}. The state I_i of each neuron in the input layer is assigned directly from the input data, whereas the states of hidden layer neurons are computed by the sigmoid function,

$h_j = 1 / (1 + \exp -(w_{j0} + \quad w_{ij} I_i))$,

where, w_{j0} is the bias weight

The back propagation algorithm was used to minimize the differences between the computed output and the desired output. Ten thousand cycles (epochs) of iterations are performed. Subsequently, the best epoch with minimum error was identified. At this point the network produces approximate target values for a given input in the training set.

A network was trained optimally for each attribute. Thus five networks were prepared. The schematic diagram (Figure 1) shows the procedure adopted. The number of neurons in the input layer was equal to the number of input data points for each attribute (for example 20 neurons for 20 numerical input vectors of the amino acid composition attribute). The optimal number of neurons in the hidden layer was determined through experimentation for minimizing the error at the best epoch for each network individually. An upper limit for the total number of weight connections was set to half of the total number of input vectors to avoid over fitting as suggested previously (Andrea *et al*).

Computer programs to compute individual compositional attributes were written in C and executed on a PC under Red Hat Linux ver 7.3 or 8.0. The network was trained on the training set, checks error and optimizes using the validate set through back propagation. The validate set was different from the training set. Since, the number of well annotated adhesins were not many, we used the 'validate set' itself as test set for preliminary evaluation of the performance and to obtain the fraction of correlation to compute the weighted average probability (P_{ad} value) described in the next section. The training set had 367 adhesins and 580 non-adhesins. The validate set had 102 adhesins and 123 non-adhesins. The adhesins were qualified with a digit '1' and the non-adhesins were qualified with a digit '0'.

During predictions, the network is fed with new data from the sequences that were not part of training set. Each network assigns a probability value of being an adhesin to a given sequence. The final probability is computed as described in the next section.

Probability of being an adhesin, the P_{ad} value

Query proteins are processed modularly through network trained for each attribute. Thus, five probability outputs are obtained. Final prediction was computed using the following expression which is a weighted linear sum of the probabilities from five modules:

$$P_{ad} = \frac{(P_A * fc_A + P_C * fc_C + P_D * fc_D + P_H * fc_H + P_M * fc_M)}{(fc_A + fc_C + fc_D + fc_H + fc_M)}$$

P_i = Probability from i module,

fc_i = fraction of correlation of i module of the trained Neural Network,

Where i = A (Amino acid frequencies), C (Charge composition), D (Dipeptide frequencies), H (Hydrophobic composition), or M (Multiplet frequencies).

The fraction of correlation fc_i represents the fraction of total entries that were correctly predicted ($P_{i,adhesin} > 0.5$ and $P_{i,\ non\text{-}adhesin} < 0.5$) by the trained network on the test set used in preliminary evaluation (Charles Anderson).

Neural Network

A feed forward error back propagation Neural Network was used. The program was downloaded from the web site with permission from the author, Charles W. Anderson, Department of Computer Science, Colorado State University, Fort Collins, CO 80523, anderson@cs.colostate.edu

Statistical Analysis

All statistical procedures were carried out using Microsoft Excel (Microsoft Corporation Inc. USA).

Sequence analysis

Homology analysis was carried out using CLUSTAL W (Thompson *et al* 1994), BLAST (Altschul *et al* 1990), CDD (conserved domain database) search (Marchler-Bauer *et al* 2002).

The whole genome sequences of microbial pathogens present new opportunities for the development of clinical applications such as diagnostics and vaccines. The present invention provides new leads for the development of candidate genes, and their encoded proteins in their functional relevance to preventive therapeutics.

The protein sequences of both the classes, i.e. adhesin and non-adhesin, were downloaded from the existing database (National Centre for Biotechnology Information (NCBI), USA). A total of 105 compositional properties under the five sequence

attributes namely, amino acid composition, multiplet composition, dipeptide composition, charge composition and hydrophobic composition were computed by computer programs written in C language. The attributes were computed for all the proteins in both the databases. The sequence-based attributes were then used to train Artificial Neural Network for each of the protein attributes. Adhesins were qualified by the digit '1' and non-adhesins were qualified by the digit '0'. Finally each trained Artificial Neural Network was used to identify potential adhesins which can be envisaged to be useful for the development of preventive therapeutics against pathogenic infections. Accordingly, the invention provides a computational method for identifying adhesin and adhesin-like proteins of therapeutic potential, which comprises:

1. preparing two comprehensive data-sets of adhesin and non-adhesin proteins from publicly available information on protein sequences,
2. calculating computationally the sequence based attributes of the protein sequences in the publicly available protein datasets using specially developed Software for Prediction of Adhesins and Adhesin-like proteins using Neural Networks (SPAAN),
3. training the Artificial Neural Network (ANN) for the selected attributes,
4. assigning probability value suitable for an adhesin, "P_{ad}" to the query protein and identifying adhesin like property in the query proteins with the help of trained Artificial Neural Network implemented in SPAAN,
5. validating computationally the protein sequences as therapeutic potentials by comparing with the known protein sequences that are biochemically characterized in the pathogen genome.

In an embodiment of the invention the protein sequence data may be taken from an organism, specifically but not limited to organisms such as *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Mycoplasma pneumoniae*, *Mycobacterium tuberculosis*, *Rickettsiae prowazekii*, *Porphyromonas gingivalis*, *Shigella flexneri*, *Streptococcus mutans*, *Streptococcus pneumoniae*, *Neisseria meningitides*, *Streptococcus pyogenes*, *Treponema pallidum*, Severe Acute Respiratory Syndrome associated coronavirus.

In another embodiment to the present invention different sequence-based attributes used for identification of proteins of therapeutic potential, comprise amino acid composition, charge composition, hydrophobicity composition, multiplets frequencies, and dipeptide frequencies.

In an embodiment, the non-homologous adhesin protein sequence may be compared with that of known sequences of therapeutic applications in the selected pathogens.

In an embodiment of the invention, the sequences of adhesin or adhesin like proteins comprise sequences of sequences IDs listed in Tables 5 and 6 identified by the method of invention.

.Another embodiment of the invention the computer system comprises a central processing unit, executing SPAAN program, giving probabilities based on different attributes using Artificial Neural Network and in built other programs of assessing attributes, all stored in a memory device accessed by CPU, a display on which the central processing unit displays the screens of the above mentioned programs in response to user inputs; and a user interface device.

In One embodiment of the present invention, the particulars of the organisms such as their name, strain, accession number in NCBI database and other details are given in Table 2:

The invention is further explained with the help of the following examples, which are given by illustration and should be construed to limit the scope of the present invention in any manner.

Example 1

Operating SPAAN:

The purpose of the program is to computationally calculate various sequence-based attributes of the protein sequences.

The program works as follows:

The internet downloaded FASTA format files obtained from http://www.ncbi.nlm.nih.gov were saved by the name <organism_name>.faa are converted in the standard format by C program and passed as input to another set of C programs which computes the 5 different attributes of protein sequences (a total of 105 compositional properties in all 5 modules).

The computed properties were fed as input to the 5 different Neural Networks. Each trained network assigns a probability value of being an adhesin for a query protein. The final probability (P_{ad}) was calculated as weighted average of these five individual probabilities. The weights were determined from a correlation value of correct prediction during test runs of each of the five modules.

Input/Output format:

Downloaded Files and their format:

<organism_name>.faa: file which stores the annotation and the protein sequence.

Input file Format: FASTA

">gi.vertline."<annotation>

For example,

>gi.vertline.2314605.vertline.gb.vertline.AAD08472.vertline.histidine and glutamine-rich protein

MAHHEQQQQQQANSQHHHHHHHAHHHHYYGGEHHHHNAQQHAEQQAEQQ
AQQQQQQQAHQQQQQKAQQQNQQY

>gi.vertline.3261822.vertline.gn1.vertline.PID.vertline.e328405 PE_PGRS

MIGDGANGGPGQPGGPGGLLYGNGGHGGAGAAGQDRGAGNSAGLIGNGGAG
GAGGNGGIGGAGAPGGLGGDGGKGGFADEFTGGFAQGGRGGFGGNGNTGAS
GGMGGAGGAGGAGGAGGLLIGDGGAGGAGGIGGAGGVGGGGGAGGTGGGG
VASAFGGGNAFGGRGGDGGDGGDGGTGGAGGARGAGGAGGAGGWLSGHSG
AHGAMGSGGEGGAGGGGGARGEAGAGGGTSTGTNPGKAGAPGTQGDSGDP
GPPG

>gi.vertline.. . .

Table 1: Output file format given by SPAAN

<organism_name>.out

SN	P_A	P_C	P_D	P_H	P_M	P_{ad}-value	Protein Name
1	0.05683	0.290803	0.441338	0.50304	0.029503	0.260485	>gi.vertline.32454344.vertline.gb.vertline.AAP82966.1. vertline.orf1a polyprotein [SARS coronavirus Hong Kong ZY-2003]
2	0.639235	0.166721	0.054583	0.935385	0.453498	0.462452	>gi.vertline.32454345.vertline.gb.vertline.AAP82967.1. vertline.orf1ab polyprotein [SARS coronavirus Hong Kong ZY-2003]
3	0.651111	0.911504	0.438696	0.543944	0.924044	0.690247	>gi.vertline.32454346.vertline.gb.vertline.AAP82968.1. vertline.spike glycoprotein [SARS coronavirus Hong Kong ZY-2003]

4	0.464324	0.655003	0.179503	0.008700	0.241573	0.300970	>gi.vertline.32454347.vertline.gb.vertline.AAP82969.1. vertline.Orf3a [SARS coronavirus Hong Kong ZY-2003]

Where P_A, P_C, P_D, P_H, P_M are the outputs of the five Neural Networks.

Example 2 organisms and sequence numbers

Table 2: Organism Name, Accession number, Number of base pairs, Date of release and Total number of proteins analyzed

Organism Name	Accession Number	Number of base pairs	Date of release	Total no. of proteins
E. coli O157 H7	NC_002695	5498450	7-Mar-2001	5361
H. influenzae Rd	NC_000907	1830138	30-Sep-1996	1709
H. pylori J99	NC_000921	1643831	10-Sep-2001	1491
M. pneumoniae	NC_000912	816394	2-Apr-2001	689
M. tuberculosis H37Rv	NC_000962	4411529	7-Sep-2001	3927
R. prowazekii strain Madrid E	NC_000963	1111523	10-Sep-2001	835
P. gingivalis W83	NC_002950	2343476	9-Sep-2003	1909
S. flexneri 2a str. 2457T	NC_004741	4599354	23- Apr-2003	4072
S. mutans UA159	NC_004350	2030921	25-Oct-2002	1960
S. pneumoniae R6	NC_003098	2038615	6-Sep-2001	2043
N. meningitidis serogroup A strain Z2491	NC_003116	2184406	27-Sep-2001	2065
S. pyogenes MGAS8232	NC_003485	1895017	Jan 31, 2002	1845
T. pallidum subsp. pallidum str. Nichols	NC_000919	1138011	7-Sep-2001	1036
Severe Acute Respiratory Syndrome (SARS) associated coronavirus Frankfurt 1	AY291315	29727	11-JUN-2003	14
SARS coronavirus HSR 1	AY323977	29751	15-OCT-2003	14

SARS coronavirus ZJ01	AY297028	29715	19-MAY-2003	3
SARS coronavirus TW1	AY291451	29729	14-MAY-2003	11
SARS coronavirus CUHK-Su10	AY282752	29736	07-MAY-2003	4
SARS coronavirus Urbani	AY278741	29727	12-AUG-2003	12
SARS coronavirus	NC_004718	29751	9-Sep-2003	29
SARS coronavirus Tor2	AY274119	29751	16-MAY-2003	15
SARS coronavirus GD01	AY278489	29757	18-AUG-2003	12
SARS coronavirus CUHK-W1	AY278554	29736	31-JUL-2003	11
SARS coronavirus BJ01	AY278488	29725	01-MAY-2003	11

Example 3

The multi-layered feed forward Neural Network architecture implemented in SPAAN (figure 1). A given protein sequence in FASTA format is first processed through the 5 modules A, C, D, H, and M to quantify the five types of compositional attributes. A: Amino acid composition, C: Charge composition, D: dipeptide composition of the 20 dipeptides (NG, RE, TN, NT, GT, TT, DE, ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI, HR), H: Hydrophobic composition, M: Amino acid frequencies as Multiplets. The sequence shown is part of the FimH precursor (gi 5524634) of *E. coli.* Subsequently, these numerical data are input to the input neuron layer. The directions of arrows show data flow. The number of neurons chosen in the input layer was equal to the number of the numerical input vectors of each module. The network was optimally trained through minimization of error of detection based on validate set through back propagation. The details are described in the methods. Each network module assigns a probability value of the protein being an adhesin based on the corresponding attribute. The final probability of a protein sequence being an adhesin is the P_{ad} value a weighted average of the individual probabilities and the associated fraction of correlation which is a measure of the strength of the prediction.

Example 4

Performance of SPAAN assessed using a test set of 37 adhesins and 37 non-adhesins that were not part of the training set. Matthew's correlation coefficient (Mcc, plotted on

Y-axis) for all the proteins with P_{ad} values above a given threshold (plotted on X-axis) (figure 2). The Matthew's correlation is defined as:

$$Mcc = \frac{(TP*TN)-(FP*FN)}{\sqrt{(TN+FN)(TN+FP)(TP+FN)(TP+FP)}}$$

Where TP = True Positives, TN = True Negatives, FP = False Positives, FN = False Negatives.

Here TPs are adhesins, TNs are non-adhesins. In general, adhesins have high P_{ad} value, whereas non-adhesins have low P_{ad} value. Thus known adhesins with P_{ad} value above a given threshold are true positives whereas known non-adhesins with P_{ad} value below the given threshold are true negatives. The sensitivity, Sn is given by $\left(\frac{TP}{TP+FN}\right)$ and specificity, Sp is given by $\left(\frac{TP}{TP+FP}\right)$. False negatives are those cases, wherein a known adhesin had P_{ad} value lower than the chosen threshold. Similarly, a known non-adhesin with a P_{ad} value higher than the chosen threshold was taken as false positive. A theoretical polynomial curve of second order (dashed line) was fitted to the observed curve (smooth line) with a Karl-Pearson correlation coefficient $R^2 = 0.9799$. The maximum point of the theoretical curve (where first derivative vanishes and second derivative is negative) was chosen as reference (vertical dotted line) to identify the maximum Mcc = 0.94 on the observed curve (shown by arrow). The corresponding P_{ad} value threshold was 0.51. At this P_{ad} value threshold, Sn and Sp were 0.89 and 1.0 respectively. Note that the Mcc does not drop down to the x-axis because the highest P_{ad} value attained by adhesins was 0.939 in comparison to the theoretical attainable limit of 1.0.

Example 5

Assessment of SPAAN on well known adhesins from various bacterial pathogens.

Table 3. Prediction of well characterized adhesins from various bacterial pathogens using SPAAN.

Species	Disease caused	Adhesin[a]	Host ligand	P_{ad} value[b] (Range)
E. coli	Diarrhoea	PapG (27)	α-D-gal(1-4) β-D-Gal-containing receptors	0.84-0.76
		SfaS (5)	alpha-sialyl-beta-2,3-b-galactose	0.94-0.94
		FimH (63)	D-mannosides	0.96-0.23[c]

		Intimin (12)	tyrosine-phosphorylated form of host cell receptor Hp90	0.95-0.78
		PrsG (5)	Gal(alpha1-4)Gal	0.86-0.85
Nontypeable *H. influenzae*	Influenza	HMW1, HMW2	Human epithelial cells	0.97
		Hia (8)	human conjuctival cells	0.93-0.90
H. influenzae	bacterial meningitis[d]	HifE (18)	Sialylyganglioside-GM1	0.85-0.73
K. pneumoniae	Pneumonia	MrkD	type V collagen	0.82
B. pertussis	Whooping cough	FHA	Sulphated sugars on cell-surface glycoconjugates	0.85
		Pertactin	Integrins	0.43
Y. enterocolitica	Enterocolitis	YadA (5)	β_1 integrins	0.88-0.79
S. mutans	Dental Caries	SpaP (2) PAc	Salivary glycoprotein Salivary glycoprotein	0.88, 0.87 0.88
Streptococcus gordonii	Oral cavity	SspA (2)	Salivary glycoprotein	0.85, 0.84
		CshA	Fibronectin	0.78
		CshB	Fibronectin	0.63
		ScaA	Co-aggregation	0.71
		SspB (2)	Salivary glycoprotein	0.85,0.84
Streptococcus sobrinus	Tooth decay	SpaA PAg (2)	Salivary glycoprotein Salivary glycoprotein	0.89 0.89, 0.73
Streptococcus pyogenes	Scarlet Fever	Protein F	Fibronectin	0.49
Streptococcus pneumoniae	Bacterial Pneumonia	PsaA (5)	Human nasopharyngeal cells	0.82-0.78
		CbpA[e] / SpsA / PbcA/ PspC	phosphorylcholine of the teichoic acid.	0.81-0.49
Streptococcus parasanguis	Valve endocarditis	FimA	Salivary glycoprotein fibrin	0.76
Streptococcus sanguis	Tooth Decay	SsaB	Salivary glycoprotein	0.71
Enterococcus faecalis	Empyma in patients with liver disease	EfaA	Unknown	0.83
Staphylococcus aureus	Food Poisoning	FnbA FnbB (3)	Fibronectin Fibronectin	0.8 0.78, 0.77, 0.69
Helicobacter pylori	Peptic Ulcers	BabA (17)	difucosylated Lewis[b] blood group antigen	0.87-0.68

[a]: The number of sequences from different strains and homologs from related species analyzed are shown in parantheses.

[b]: Rounded off to the second decimal.

[c]: Out of 63 FimH proteins, 54 were from *E. coli*, 6 from *Shigella flexineri*, 2 from *Salmonella enterica* and 1 was from *Salmonella typhimurium*. Except 2 FimH proteins, the rest had P_{ad} 0.51. The 2 exceptions (gi numbers: 5524636, 1778448) were from *E. coli*. The gi:5524636 protein is annotated as a FimH precursor but is much shorter (129 amino acids) than other members of the family. The gi:1778448 protein is a *S. typhimurium* homolog in *E. coli*.

[d]: Other ailments include pneumonia, epiglottitis, osteomyelitis, septic arthritis and sepsis in infants and older children.

[e]: The adhesin CbpA is also known by alternative names SpsA, PbcA and PspC. A total of seven sequences were analyzed. Except 1 PspC sequence, the rest all had P_{ad} 0.51.

Example 6

Ability of SPAAN to discriminate adhesins from non-adhesins at Pad 0.51 (figure 3-a).

Example 7

The non-homology character of SPAAN assesses in both adhesins and non-adhesins (figure 3b and 3c).

Figure 3 (a – c). SPAAN is non-homology based software. A total of 130 adhesins and 130 non-adhesins were analyzed to assess whether the predictive power of SPAAN could be influenced by the sequence relationships. (a) Histogram plots of the number of proteins in the various P_{ad} value ranges are shown. Shaded bars represent adhesins whereas open bars represent non-adhesins. Note the SPAAN's ability to segregate adhesins and non-adhesins into two distinct cohesive groups. (b) Pairwise sequence relationships among the adhesins were determined using CLUSTAL W and plotted on X-axis. Higher scores indicate similar pairs. The corresponding differences in P_{ad} values in the same protein pair was plotted on the Y-axis. Each point in the diagram represents a pair. Arrow points to protein pairs of the FimH family with high ΔP_{ad} values in spite of high similarity. Since one of the FimH proteins (gi: 5524636) had very low P_{ad} value all pairs with this false negative protein show high ΔP_{ad} values. The protein (gi: 5524636) is of much shorter length compared with other members of the same family. (c) plot for non-adhesins. Data are plotted in the 4 quadrant format for clear inspection. Note that among protein pairs with CLUSTAL W score < 20 the majority (82% in adhesins and 86% in non-adhesins) have $\Delta P_{ad} < 0.2$. These data support the non-homology character of SPAAN.

Example 8

Genomescan of pathogens by SPAAN identifies well known adhesins and new adhesins and adhesin-like proteins

Table 4. Analysis of predictions made by SPAAN on genome scans of a few selected pathogenic organisms[a]

Species / Protein Class	*Escherichia coli* O157:H7	*Mycobacterium tuberculosis* H37Rv	SARS associated corona virus (11 strains)
Total number of proteins with P_{ad} 0.51	575	435	5
Known adhesins	17[b]	-	-
Putative proteins with adhesin like characteristics	92[c]	105[j]	-
Hypothetical proteins with adhesin-like characteristics	22[d]	-	-
Proteins likely to be extracytoplasmic or located at surface	190[e]	191[k]	5[m]
Phage proteins	30[f]	-	-
Others	13[g]	6[l]	-
Hypothetical proteins	157[h]	86[h]	-
Wrong predictions	54[i]	47[i]	-

[a]: SPAAN has general applicability. The three pathogens chosen here are those in which intense investigations are being conducted presently. *M. tuberculosis* is of special importance to developing countries.

[b]: Fimbrial adhesins, AidA-I, gamma intimin, curlin, translocated intimin receptor, putative adhesin and transport, Iha, prepilin peptidase dependent protein C.

[c]: These proteins have been annotated as proteins with a putative function. These sequences were analyzed using CDD (Conserved domain database, NCBI) and BLAST searches. Adhesin like domains were found in these proteins.

[d]: These proteins have been annotated as 'hypothetical'. These sequences were analyzed using CDD and BLAST searches. Adhesin like domains were found in these proteins.

[e]: These proteins are outer membrane, extracellular, transport, surface, exported, flagellar, periplasmic lipoprotein, and proteins annotated as 'hypothetical' but found to have similar functions listed here using BLAST and CDD searches.

[f]: The phage proteins were of the following functional roles – tail fiber, head decoration, DNA injection, tail, major capsid, host specificity, endolysin.

[g]: Proteins predicted by SPAAN but not readily classifiable into the classes listed here have been collectively grouped as 'Others'. However, some of these proteins are known to participate in host-pathogen interactions. The annotated functional roles are typeIII secretion, antibiotic resistance, heat shock, acid shock, structural, tellurium resistance, terminase, Hcp-like, Sec-independent translocase, uncharacterized nucleoprotein, HicB-like.

[h]: These proteins have been annotated as hypothetical. Re-analyses of these proteins using BLAST and CDD failed identify any function for these proteins.

[i]: These proteins have been annotated with functional roles that are very likely to occur within the cell. Hence these proteins may have remote possibility of functioning as adhesins or adhesin-like proteins. Therefore this set of proteins have been incorrectly predicted as adhesins or adhesin-like by SPAAN.

[j]: These proteins are PE_PGRS, PE proteins. Several reports (for example Brennan *et al.*) indicate that PE_PGRS proteins may be localized to cell surface and aid in host-pathogen interaction.

[k]: Lipoproteins (lpp, lpq, lpr), PPE, outer membrane, surface, transport, secreted, periplasmic, extracellular, ESAT-6, peptidoglycan binding, exported, mpt (with extracellular domains), and proteins annotated as 'hypothetical' but found to have similar functions listed here using BLAST and CDD searches.

[l]: These proteins were of the following functions - glutaredoxin-like thioltransferase, putative involvement in molybdate uptake, ATP synthase chain, sulphotransferases, S.erythraea rhodanese-like protein M29612|SERCYSA_5, unknown function.

[m]: These proteins were the spike glycoprotein with antigenic properties, and nsp2, nsp5, nsp6 and nsp7.

Table 5: New putative adhesins predicted by SPAAN in the genomes listed in table 2 –

(Total number = 279)

Protein GI Number	Gene ID	Protein name
Escherichia coli O157:H7		
13360742	912619	hemagglutinin/hemolysin-related protein
13362986	914770	putative ATP-binding component of a transport system
13361114	913228	putative tail fiber protein
13364757	913676	minor fimbrial subunit/D-mannose specific adhesin
13362687	915687	putative fimbrial-like protein
13360856	912599	AidA-I adhesin-like protein
13364140	915374	putative fimbrial protein
13359793	914435	putative invasin
13364768	913650	putative invasin
13364034	915471	Gamma intimin
13362703	915668	putative DNA transfer protein precursor
13364141	915376	putative fimbrial protein
13359819	914463	AidA-I adhesin-like protein
13360480	917768	putative fimbrial-like protein
13362692	915681	putative fimbrial-like protein
13362585	916824	putative ATP-binding component of a transport system
13359881	914526	putative flagellin structural protein
13361579	917311	putative type 1 fimbrial protein precursor
13360880	913991	curlin major subunit CsgA
13364036	915465	translocated intimin receptor Tir
13360740	912615	putative major pilin protein
13361582	917317	putative ATP-binding component of a transport system and adhesin protein
13364754	913683	export and assembly outer membrane protein of type 1 fimbriae
13360484	917767	homolog of Salmonella FimH protein

13364751	913688	major type 1 subunit fimbrin
13359597	913742	putative fimbrial protein
13362550	916787	putative ATP-binding component of a transport system
13359595	913739	putative fimbrial protein
13359599	913748	probable outer membrane porin protein involved in fimbrial assembly
13363900	915704	putative fimbrial protein precursor
13361575	917307	putative fimbrial-like protein
13364756	913678	fimbrial morphology
13363496	916142	truncated putative fimbrial protein
13359601	913761	putative fimbrial-like protein
13364145	915368	putative type 1 fimbrial protein
13363902	915708	putative outer membrane usher protein precursor
13361576	917309	putative outer membrane protein
13361013	913353	putative major tail subunit
13364755	913682	fimbrial morphology
13360738	912793	putative outer membrane usher protein
13363928	915608	alpha-amylase
13363495	916144	putative outer membrane protein
13362383	916617	putative type-1 fimbrial protein
13364373	914972	outer membrane vitamin B12 receptor protein BtuB
13360879	912479	minor curlin subunit precursor CsgB
13360739	912756	putative chaperone protein
13361574	917314	putative fimbrial-like protein
13361127	913212	outer membrane protease precursor
13363210	916442	putative lipoprotein
13361104	913238	major tail protein
13361709	917446	putative major tail subunit
13359725	914366	outer membrane pore protein PhoE
13360875	913765	curli production assembly/transport component CsgF
13362170	913927	putative outer membrane protein
13361473	917203	putative BigB-like protein

13364025	915286	EspF protein
13360081	916982	outer membrane receptor for ferric enterobactin (enterochelin) and colicins B and D
13362977	914779	hypothetical lipoprotein
13360351	917632	outer membrane protein X
13360696	914208	putative outer membrane precursor
13361456	917206	putative outer membrane protein
13361626	917374	putative outer host membrane protein precursor
13361698	917449	putative outer membrane protein
13362186	913421	putative outer membrane protein precursor
13362697	915676	long-chain fatty acid transport protein FadL
13360918	914188	flagellar hook protein FlgE
13360737	912506	putative outer membrane protein
13360342	917629	putative outer membrane receptor for iron transport
13363396	916248	outer membrane channel TolC
13361958	912705	putative scaffolding protein in the formation of a murein-synthesizing holoenzyme
13359921	914566	nucleoside-specific channel-forming protein TSX
13360944	913890	outer membrane receptor for ferric iron uptake
13359998	914644	putative outer membrane transport protein
13363390	916251	putative ferrichrome iron receptor precursor
13364227	915153	outer membrane phospholipase A
13361982	912846	putative outer membrane protein
13360129	917032	a minor lipoprotein
13361817	912692	putative outer membrane protein
13360233	917507	membrane spanning protein TolA
13362837	915218	putative outer membrane lipoprotein
13362328	912985	putative colanic acid biosynthesis glycosyl transferase
Haemophilus influenzae Rd		
16272254	949521	prepilin peptidase-dependent protein D
16272928	950762	immunoglobin A1 protease
16272129	951072	lipoprotein

16273251	950616	hemoglobin-binding protein
30995429	950130	opacity protein
16272854	949634	protective surface antigen D15
16272283	950648	opacity associated protein
16272604	949701	hemoglobin-binding protein
Helicobacter pylori J99		
4155101	889167	putative vacuolating cytotoxin (VacA) paralog
4154798	890022	putative vacuolating cytotoxin (VacA) paralog
4155426	890036	putative vacuolating cytotoxin (VacA) paralog
4155390	890075	vacuolating cytotoxin
4155400	890058	outer membrane protein - adhesin
4155681	889718	putative Outer membrane protein
4155420	890042	Outer membrane protein/porin
4155775	889799	outer membrane protein - adhesin
4155419	890044	Outer membrane protein/porin
4154526	889066	putative Outer membrane protein
4154724	889419	putative Outer membrane protein
4155862	890404	putative Outer membrane protein
4156048	889958	putative IRON(III) DICITRATE TRANSPORT PROTEIN
4154510	889297	putative Outer membrane protein
4155432	889515	putative outer membrane protein
4155623	889671	putative Outer membrane protein
4155700	889739	putative Outer membrane function
4154740	889426	Outer membrane protein/porin
4155692	889743	putative Outer membrane protein
4155594	889648	putative outer membrane protein
4155680	889719	putative Outer membrane protein
4155217	890243	putative Outer membrane protein
4155958	889905	putative Outer membrane protein
4155201	890259	putative Outer membrane protein
4155013	889232	cag island protein
4154974	889032	putative Outer membrane protein

4155214	890244	putative Outer membrane protein
4154973	889042	Outer membrane protein
4155344	890115	putative Outer membrane protein
4155099	889160	FLAGELLIN A
4155023	888978	cag island protein
4155035	889201	cag island protein, CYTOTOXICITY ASSOCIATED IMMUNODOMINANT ANTIGEN
4155289	890164	NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ PRECURSOR
Mycoplasma pneumoniae		
13507881	877207	involved in cytadherence
13507880	877268	ADP1_MYCPN adhesin P1
13508228	877211	species specific lipoprotein
13508181	877124	species specific lipoprotein
13508179	877071	Mollicute specific lipoprotein, MG307 homolog, from M. genitalium
13508178	877118	Mollicute specific lipoprotein, MG307 homolog, from M. genitalium,
13508176	876797	Mollicute specific lipoprotein, MG307 homolog, from M. genitalium
13508175	876848	Mollicute specific lipoprotein, MG307 homolog, from M. genitalium
13508106	876953	involved in cytadherence
13508350	877112	similar to phosphate binding protein Psts
Mycobacterium tuberculosis H37 Rv		
15607496	886491	PPE
15607445	886592	PPE
15610644	888270	PE_PGRS
15608588	886605	PE_PGRS
15609627	887941	PE_PGRS
15610643	888256	PE_PGRS
15607718	887725	PE_PGRS

15609054	885362	PPE
15610486	888113	PPE
15610483	888120	PPE
15610479	888033	PPE
15609771	888573	PE_PGRS
15610648	888306	PE_PGRS
15610481	888114	PE_PGRS
15608117	885264	PE_PGRS
15607973	885391	PE_PGRS
15608231	885258	PE_PGRS
15608906	885429	PE_PGRS
15608891	885544	PPE
15609990	888171	PE_PGRS
15609055	885506	PPE
15608227	887094	PE_PGRS
15610524	888151	PE_PGRS
15609490	886003	PPE
15607886	888664	PE_PGRS
15609624	887909	PE_PGRS
15607420	886621	PE_PGRS
15608897	885325	PE_PGRS(wag22)
15608590	886595	PE_PGRS
15609728	887992	PE_PGRS
15608012	885742	PE_PGRS
15608534	886745	PE_PGRS
15608940	885730	PE_PGRS
15607887	888662	PE_PGRS
15609235	888312	PE_PGRS
15610694	887822	PPE
15609533	885517	PE_PGRS
15610480		PE_PGRS

Rickettsia prowazekii strain Madrid E

15604316	883411	CELL SURFACE ANTIGEN (sca3)
15604546	883694	CELL SURFACE ANTIGEN (sca5)
Porphyromonas gingivalis W83		
34541453	2551934	hemagglutinin protein HagA
34540040	2551409	lipoprotein, putative
34540364	2552375	extracellular protease, putative
34541613	2552074	hemagglutinin protein HagE
34540183	2551891	internalin-related protein
Shigella flexneri 2a str. 2457T		
30065424	1080663	minor fimbrial subunit, D-mannose specific adhesin
30062726	1077662	putative adhesion and penetration protein
30063758	1078834	putative fimbrial-like protein
30065431	1080671	major type 1 subunit fimbrin (pilin)
30063366	1078379	flagellar protein FliD
30064308	1079668	outer membrane fluffing protein
30062613	1077555	flagellar hook protein FlgE
30061954	1076843	conserved hypothetical lipoprotein
30065173	1080393	putative lipase
30065425	1080664	minor fimbrial subunit, precursor polypeptide
30064485	1079637	putative fimbrial protein
30062615	1077558	flagellar basal body L-ring protein FlgH
30064307	1079452	outer membrane fluffing protein
30065601	1080859	putative glycoprotein/receptor
30062118	1077025	putative fimbrial-like protein
30064099	1079223	lipoprotein
30062616	1077559	flagellar basal body P-ring protein FlgI
30063546	1078596	putative fimbrial-like protein
30062940	1077910	putative outer membrane protein
30065426	1080665	minor fimbrial subunit, precursor polypeptide
30062779	1077721	putative outer membrane protein
30064194	1079329	putative lipoprotein
30063365	1078378	flagellin

30062298	1077222	outer membrane protein X
30064968	1080175	putative major fimbrial subunit
30061858	1076740	outer membrane pore protein E (E,Ic,NmpAB)
30062178	1080410	minor lipoprotein
30062479	1077412	putative fimbrial-like protein
30062565	1077506	minor curlin subunit precursor
30063880	1078972	putative outer membrane lipoprotein
30064531	1079686	cytoplasmic membrane protein
30065033	1080243	putative receptor protein
Streptococcus mutans UA159		
24378550	1029610	putative secreted antigen GbpB/SagA; putative peptidoglycan hydrolase
24379087	1028055	cell surface antigen SpaP
24380463	1029310	putative membrane protein
24379075	1028046	penicillin-binding protein 2b
24378955	1027967	penicillin-binding protein 1a; membrane carboxypeptidase
24379801	1028662	glucan-binding protein C, GbpC
24379528	1029536	hypothetical protein; possible cell wall protein, WapE
24379231	1028158	putative glucan-binding protein D; BglB-like protein
24380488	1029325	conserved hypothetical protein; possible transmembrane protein
24380291	1029139	putative amino acid binding protein
24379342	1028247	putative penicillin-binding protein, class C; fmt-like protein
24380047	1028904	putative ABC transporter, branched chain amino acid-binding protein
24378698	1029755	putative ABC transporter, metal binding lipoprotein; surface adhesin precursor; saliva-binding protein; lipoprotein receptor LraI (LraI family)
24378708	1029768	putative transfer protein
24379427	1028331	cell wall-associated protein precursor WapA
24379272	1028196	putative amino acid transporter, amino acid-binding protein
24379641	1028511	putative ABC transporter, amino acid binding protein

Streptococcus pneumoniae R6

15902395	934801	Choline-binding protein
15902381	934810	Choline-binding protein F
15902165	932894	Surface protein pspA precursor
15904047	934859	Choline binding protein D
15904036	933487	Choline binding protein A
15903986	933069	Choline-binding protein
15903796	933669	Autolysin (N-acetylmuramoyl-L-alanine amidase)

Neisseria meningitidis Z2491

15794121	907145	putative membrane protein
15794144	907168	putative surface fibril protein
15793284	906275	truncated pilin
15793460	906456	IgA-specific serine endopeptidase
15793282	906273	fimbrial protein precursor (pilin)
15793337	906332	adhesin
15793253	906243	putative lipoprotein
15794356	907848	putative lipoprotein
15793684	906699	putative membrane protein
15793290	906281	truncated pilin
15793283	906274	truncated pilin
15793475	906471	haemoglobin-haptoglobin-utilization protein
15793406	906401	porin, major outer membrane protein P.I
15794985	907333	adhesin MafA2
15794344	907836	putative lipoprotein
15794622	908118	hypothetical outer membrane protein
15793599	906604	pilus-associated protein
15793763	906779	putative periplasmic binding protein

Streptococcus pyogenes MGAS8232

19745214	995235	putative secreted protein
19746570	994224	putative penicillin-binding protein 1a
19745593	994771	putative 42 kDa protein
19745813	993958	putative adhesion protein

19745225	994839	putative choline binding protein
19745828	995250	streptolysin S associated protein
19746229	995021	putative minor tail protein
19746909	994105	putative laminin adhesion
19745560	995061	putative cell envelope proteinase
Treponema pallidum subsp. pallidum str. Nichols		
15639714	2611034	flagellar hook protein (flgE)
15639609	2611657	tpr protein J (tprJ)
15639111	2610909	tpr protein C (tprC)
15639125	2610968	tpr protein D (tprD)
SARS coronavirus		
31581505		spike protein S [SARS coronavirus Frankfurt 1]
32187357		spike protein S [SARS coronavirus HSR 1]
32187342		spike glycoprotein [SARS coronavirus ZJ01]
30698329		putative spike glycoprotein S [SARS coronavirus TW1]
30421454		putative spike glycoprotein [SARS coronavirus CUHK-Su10]
30027620		S protein [SARS coronavirus Urbani]
29836496	1489668	E2 glycoprotein precursor; putative spike glycoprotein [SARS coronavirus]
30795145		spike glycoprotein [SARS coronavirus Tor2]
31416295		spike glycoprotein S [SARS coronavirus GD01]
30023954		putative E2 glycoprotein precursor [SARS coronavirus CUHK-W1]
30275669		spike glycoprotein S [SARS coronavirus BJ01]
29837498		3C-like proteinase nsp5-pp1a/pp1ab (3CL-PRO) [SARS coronavirus]
29837501		putative nsp8-pp1a/pp1ab [SARS coronavirus]
29837503		putative nsp10-pp1a/pp1ab; formerly known as growth-factor-like protein [SARS coronavirus]
29837502		putative nsp9-pp1a/pp1ab [SARS coronavirus]

Table 6: Hypothetical proteins predicted as putative adhesins by SPAAN in the genomes listed in table 2 –

(Total number of proteins = 105)

Protein GI number	Gene ID
Escherichia coli O157:H7	
13363955	915578
13360000	914929
13362244	912369
13359999	914888
13361583	917316
13361172	913156
13361131	913207
13359780	914422
13360571	912499
13362197	912893
13362260	912399
13360947	913505
13361464	917196
13361635	917367
13362421	916655
13361463	917195
Haemophilus influenzae Rd	
16272115	951058
30995442	950581
Helicobacter pylori J99	
4155526	889586
4155712	889748
4155632	889684
4156035	889468
4155499	

Mycoplasma pneumoniae

13507870	877230
13508239	877245
13508109	876868
13508025	877084
13507838	876784
13507883	877183
13507871	877239
13507944	877056
13508241	876750
13507942	877055
13507840	877387
13507867	877242
13508201	877044
13507941	876985
13508114	877397

Mycobacterium tuberculosis H37Rv

15611014	886198
15610173	887320
15609513	885515
15608094	885411
15610958	886155
15607528	886436
15607678	887473
15609587	885760
15610708	887227
15609526	885246
15611033	886225
15609028	885094
15607730	887771
15609121	885813
15608255	885951

15608409	887039
15609124	885815
15607734	887797

Rickettsia prowazekii strain Madrid E

15604649	883964
15604322	883472
15604659	883996
15604417	883217

Porphyromonas gingivalis W83

34540233	2551594

Shigella flexneri 2a str. 2457T

30062687	1077638
30062956	1080449
30063681	1078754
30065435	1080675
30063891	1078983
30063211	1078195
30065233	1080463
30064387	1079531
30062638	1077590
30065236	1080466
30061839	1076721

Streptococcus mutans UA159

24378864	1029452
24380475	1029319
24380237	1029088
24379203	1028139
24380480	1029320
24379275	1029489
24379291	1028216
24379295	1028215
24379804	1028663

24379162	1029417
24378987	1029363
24379179	1028118
24379166	1028107
24378827	1029444
24380216	1029067
Streptococcus pneumoniae R6	
15902140	932867
15903446	934616
15903916	934001
15903848	933609
15902832	934332
15902372	934804
15902152	932889
Neisseria meningitidis Z2491	
15793668	906680
15794714	907603
Streptococcus pyogenes MGAS8232	
19747011	993608
19747024	994165
19747012	994373
19746396	995057
19746651	993824
19745883	995045
19745912	994077
Treponema pallidum subsp. pallidum str. Nichols	
15639844	2611061
15639720	2611059

Table 7: The list of 198 adhesins found in bacteria

PapG (E. coli)	
	12837502
	7407201

7407207
7407205
147096
4240529
7407203
42308
7443327
78746
18265934
26111419
26250987
26109826
26249418
13506767
42301
78745
129622
147092
13506906
7407209
147080
281926
7407199
147100
78744

SfaS (E.coli)

477910
264035
42959
134449
96425

FimH (E.coli)

26251208
26111640
5524634
29422425
5524630
29422435
29422415
10946257
29422419
11120564
29422457
11120562
29422459
5524632
29422455
29422453
29422451
29422449
29422447
29422445
29422443
29422437
29422433
29422431
29422429
29422427
29422423
29422421
29422417
729494
1361011
1790775

3599571

29422441

12620398

29422439

5524628

1787779

1742472

1742463

15801636

25321294

12515169

11120566

24051859

24112911

13360484

15800801

15830279

25392018

25500156

12514120

1787173

16128908

16501811

16759519

24051219

24112354

30040724

30062478

6650093

5524636

1778448

Intimin (E.coli)

17384659
4388530
1389879
15723931
4323336
4323338
4323340
4323342
4323344
4323346
4323348
4689314

PrsG (E.coli)

42523
42529
7443328
7443329
1172645

HMW1 (Nontypeable *H. influenzae)*

282097

HMW2 (Nontypeable H. influenzae)

5929966

Hia (Nontypeable H. influenzae)

25359682
25359489
25359709
25359628
25359414
25359389
21536216
25359445

HifE (H. influenzae)

13506868
13506870
13506872
13506874
13506876
3688787
3688790
3688793
2126301
1170264
1170265
533127
535169
3025668
3025670
3025672
3025674
642038

MrkD (K. pneumoniae)

127307

FHA (B. pertussis)

17154501

Pertactin (B. pertussis)

33571840

YadA (Y. enterocolitica)

10955604
4324391
28372996
23630568
32470319

SpaP (S. mutans)

26007028

47267

PAc (S. mutans)

129552

SspA (Streptococcus gordonii)

25990270

1100971

CshA (Streptococcus gordonii)

457707

CshB (Streptococcus gordonii)

18389220

ScaA (Streptococcus gordonii)

310633

SspB (Streptococcus gordonii)

25055226

3220006

SpaA (Streptococcus sobrinus)

546643

PAg (Streptococcus sobrinus)

217036

47561

Protein F (Streptococcus pyogenes)

19224134

PsaA (Streptococcus pneumoniae)

18252614

7920456

7920458

7920460

7920462

CbpA[e] / SpsA / PbcA/ PspC
(Streptococcus pneumoniae)

14718654

2425109

2576331

2576333

3153898

9845483

19548141

FimA (Streptococcus parasanguis)

97883

SsaB (Streptococcus sanguis)

97882

EfaA (Enterococcus faecalis)

493017

FnbA (Staphylococcus aureus)

120457

FnbB (Staphylococcus aureus)

581562

21205592

13702452

BabA (Helicobacter pylori)

13309962

13309964

13309966

13309968

13309970

13309972

13309974

13309976

13309978

13309980

13309982

13309984

13309986

13309988

13309990
13309992
13309994

Advantages:

1. The method helps in discovering putative adhesins, which are of great importance in drug discoveries and preventive therapeutics.
2. The method is useful in predicting the adhesive nature of even unique proteins, because it is independent of the homology of the query proteins with other proteins.
3. This method is easy to use. For calculating the output, only the amino acid sequence is required as input. No other information is required to get the information about its adhesive nature.

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Claims

1. A computational method for identifying adhesin and adhesin-like proteins, said method comprising steps of:
   a. computing the sequence-based attributes of protein sequences using five attribute modules of a neural network software, wherein the attributes are, (i) amino acid frequencies, (ii) multiplet frequency, (iii) dipeptide frequencies, (iv) charge composition, and (v) hydrophobic composition,
   b. training a artificial neural Network (ANN) for each of the computed five attributes, and
   c. identifying the adhesin and adhesin-like proteins having probability of being an adhesin (P_{ad}) as ≥ 0.51.
2. A method as claimed in claim 1, wherein the protein sequences are obtained from pathogens, eukaryotes, and multicellular organisms.
3. A method as claimed in claim 1, wherein the protein sequences are obtained from the pathogens selected from a group of organisms comprising *Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Mycoplasma pneumoniae, Mycobacterium tuberculosis, Rickettsiae prowazekii, Porphyromonas gingivalis, Shigella flexneri, Streptococcus mutans, Streptococcus pneumoniae, Neisseria meningitides, Streptococcus pyogenes, Treponema pallidum* and Severe Acute Respiratory Syndrome associated human coronavirus (SARS).
4. A method as claimed in claim 1, wherein the method is a non-homology method.
5. A method as claimed in claim 1, wherein the method uses 105 compositional properties of the sequences.
6. A method as claimed in claim 1, wherein the method shows sensitivity of at least 90%.
7. A method as claimed in claim 1, wherein the method shows specificity of 100%.
8. A method as claimed in claim 1, wherein the method helps identifies adhesins from distantly related organisms.
9. A method as claimed in claim 1, wherein the neural network has multi-layer feed forward topology, consisting of an input layer, one hidden layer, and an output layer.

10. A method as claimed in claim 9, wherein the number of neurons in the input layer are equal to the number of input data points for each attribute.

11. A method as claimed in claim 1, wherein the "P_{ad}" is a weighted linear sum of the probabilities from five computed attributes.

12. A method as claimed in claim 1, wherein each trained network assigns a probability value of being an adhesin for the protein sequence.

13. A computer system for performing the method of claim 1, said system comprising a central processing unit, executing SPAAN program, giving probabilities based on different attributes using Artificial Neural Network and in built other programs of assessing attributes, all stored in a memory device accessed by CPU, a display on which the central processing unit displays the screens of the above mentioned programs in response to user inputs; and a user interface device.

14. A set of 274 annotated genes encoding adhesin and adhesin-like proteins, having SEQ ID Nos. 385 to 658.

15. A set of 105 hypothetical genes encoding adhesin and adhesin-like proteins, having SEQ ID Nos. 659 to 763.

16. A set of 279 annotated adhesin and adhesin-like proteins of SEQ ID Nos. 1 to 279.

17. A set of 105 hypothetical adhesin and adhesin-like proteins of SEQ ID Nos. 280 to 384.

18. A fully connected multilayer feed forward Artificial Neural Network based on the computational method as claimed in claim 1, comprising of an input layer, a hidden layer and an output layer which are connected in the said sequence, wherein each neuron is a binary digit number and is connected to each neuron of the subsequent layer for identifying adhesin or adhesin like proteins, wherein the program steps comprise:-

[a] feeding a protein sequence in FASTA format;

[b] processing the sequence obtained in step [a] through the 5 modules named A, C, D, H and M, wherein attribute A represents an amino acid composition, attribute C represents a charge composition, attribute D represents a dipeptide composition of the 20 dipeptides [NG, RE, TN, NT, GT, TT, DE, ER, RR, RK, RI, AT, TS, IV, SG, GS, TG, GN, VI

and HR], attribute H represents a hydrophobic composition and attribute M represents amino acid frequencies in multiplets to quantify 5 types of compositional attributes of the said protein sequence to obtain numerical input vectors respectively for each of the said attributes wherein the sum of numerical input vectors is 105;

[c] processing of the numerical input vectors obtained in step [b] by the input neuron layer to obtain signals, wherein the number of neurons is equal to the number of numerical input vectors for each attribute;

[d] processing of signals obtained from step [c] by the hidden layer to obtain synaptic weighted signals, wherein the optimal number of neurons in the hidden layer was determined through experimentation for minimizing the error at the best epoch for each network individually;

[e] delivering synaptic weighted signals obtained from step [d] to the output layer for assigning of a probability value for each protein sequence fed in step [a] as being an adhesin by each network module; and

[f] using the individual probabilities obtained from step [e] for computing the final probability of a protein sequence being an adhesin denoted by the P_{ad} value, which is a weighted average of the individual probabilities obtained from step [e] and the associated fraction of correlation which is a measure of the strength of the prediction.

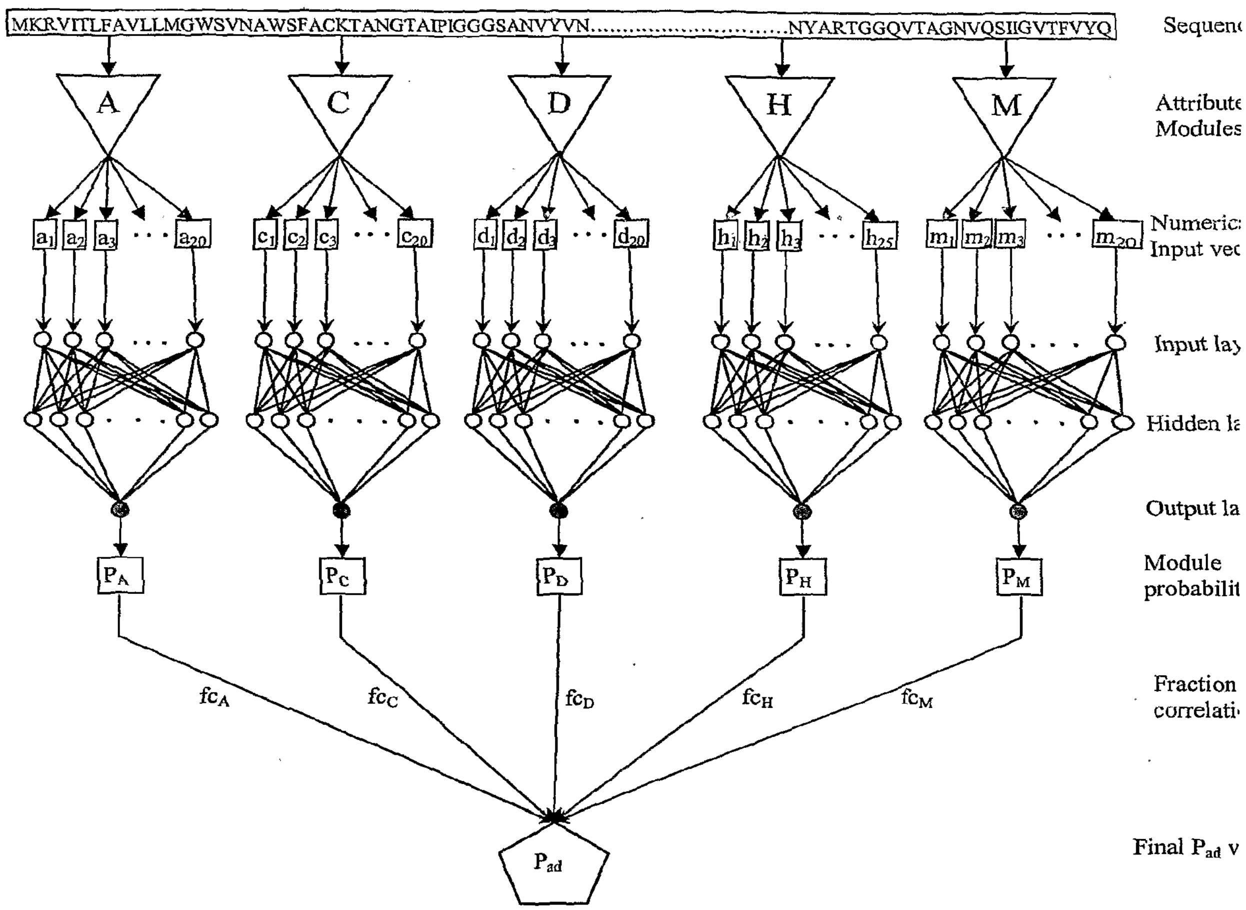
19. A network as claimed in claim 18, wherein the input neuron layer consists of a total of 105 neurons corresponding to 105 compositional properties.

20. A network as claimed in claim 18, wherein the hidden layer comprises of neurons represented as 30 for amino acid frequencies, 28 for multiplet frequencies, 28 for dipeptide frequencies, 30 for charge composition and 30 for hydrophobic composition.

21. A network as claimed in claim 18, wherein the output layer comprises of neurons to deliver the output values as probability value for each protein sequence.

The Neural Network architecture

Figure1



Assessment of SPAAN using defined test dataset.

Figure 2

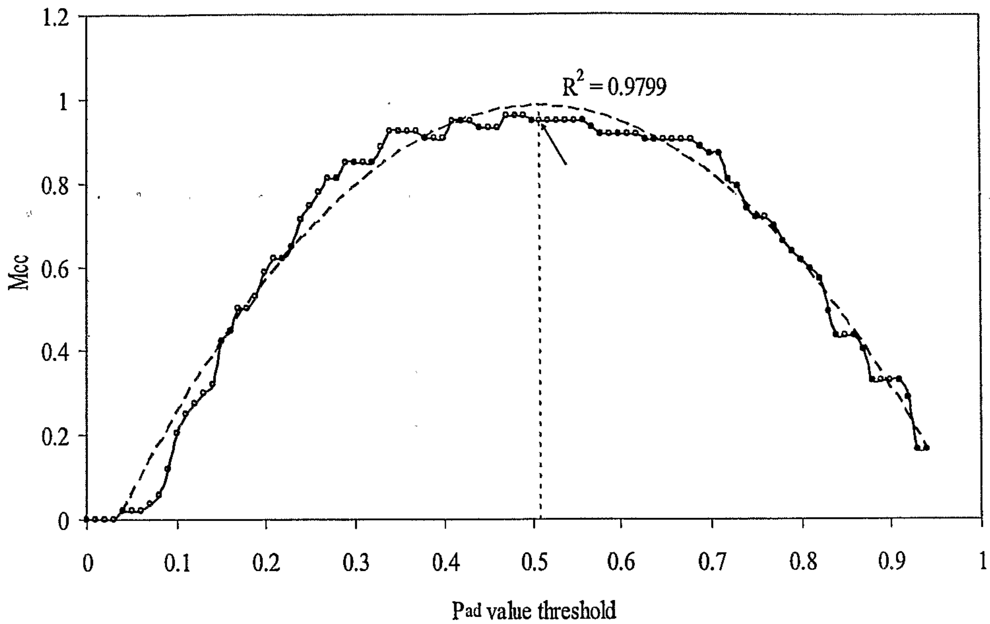
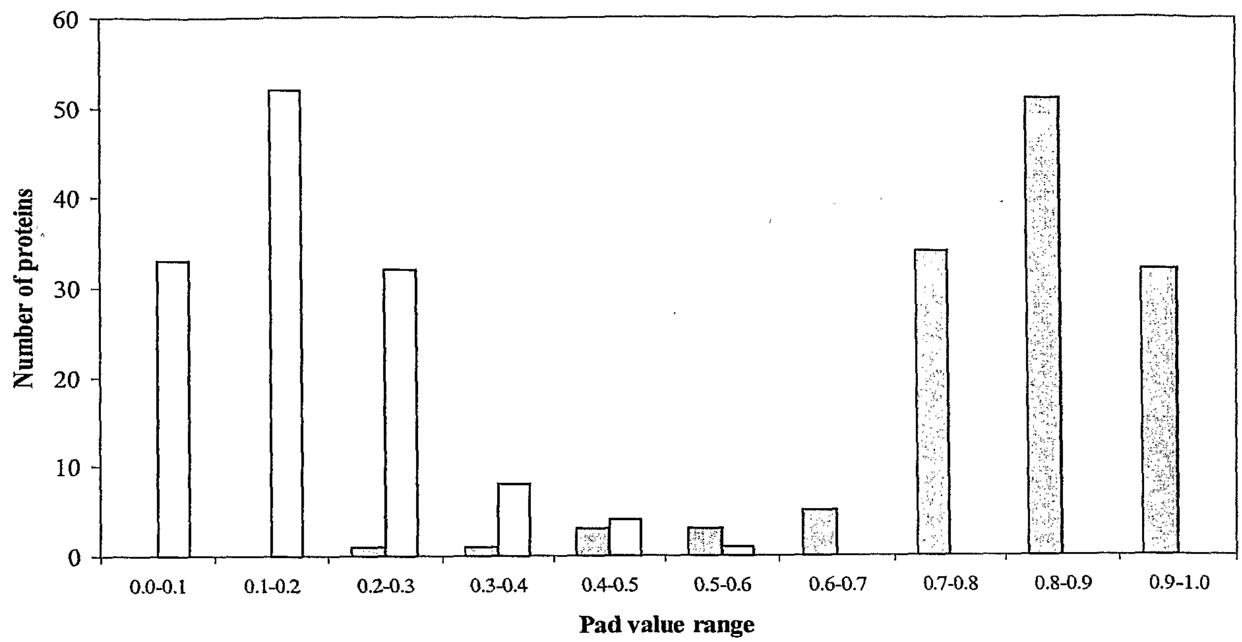


Figure 3 (a)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50
40
30
20
10
0
Number of proteins
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0.1-0.2
0.2-0.3
0.3-0.4
0.4-0.5
0.5-0.6
0.6-0.7
0.7-0.8
0.8-0.9
0.9-1.0
Pad value range

Figure 3 (b)

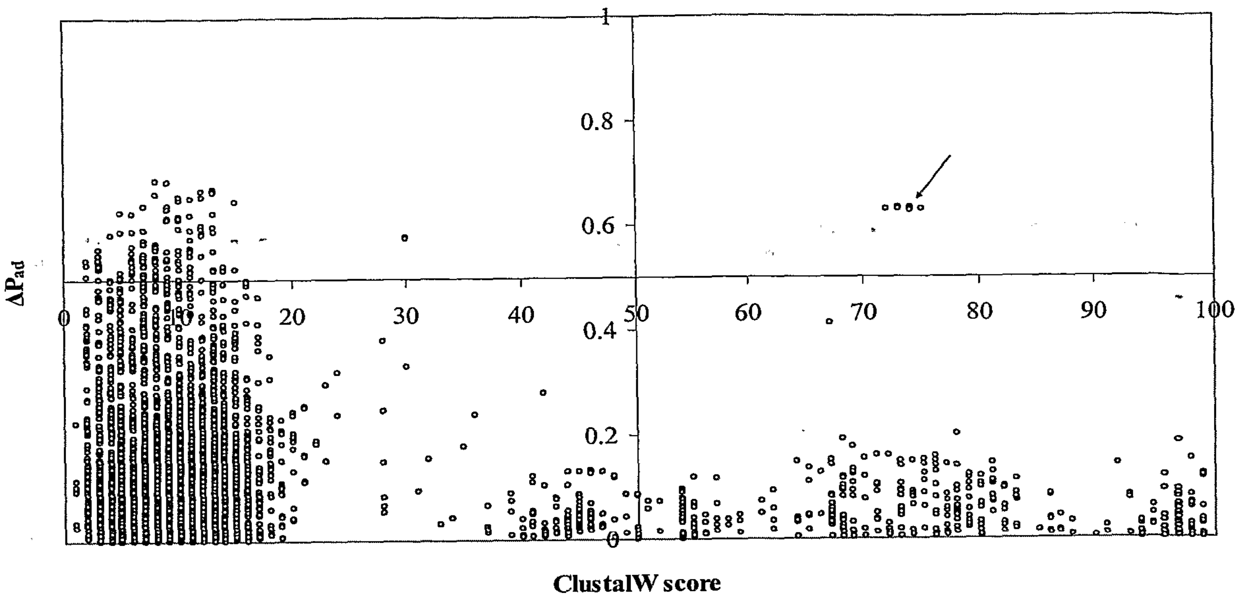
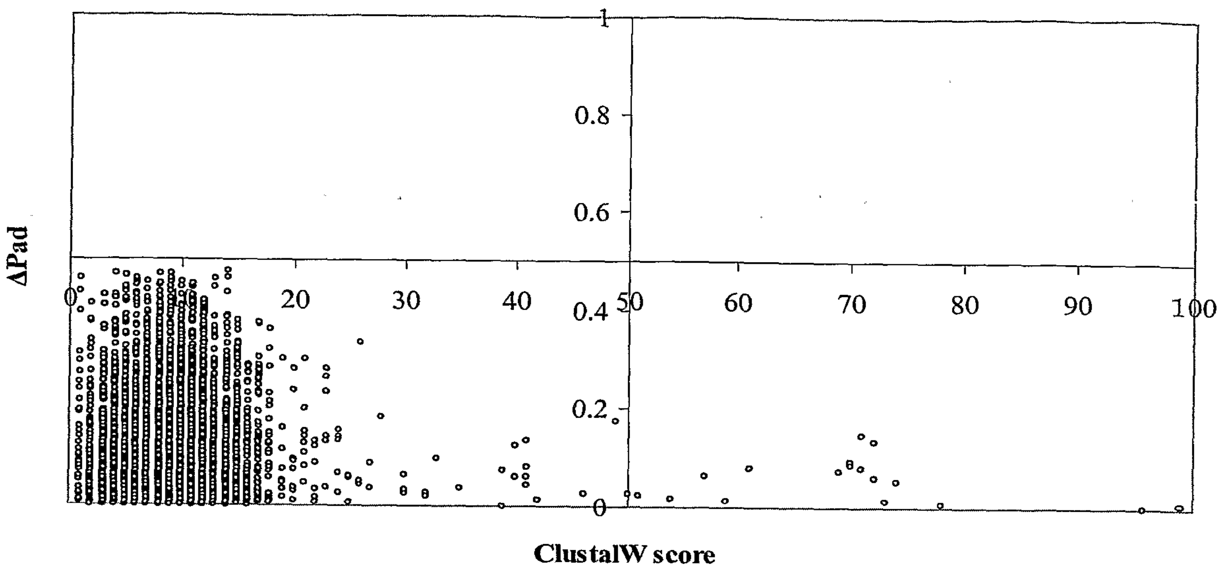

1
0.8
0.6
0.4
0.2
0
0
10
20
30
40
50
60
70
80
90
100
ΔP_{ad}
ClustalW score

Figure 3(c)



Application Project

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SDITLTPKDI GTLNSTTMSF SGGAGWFKLA TVTMPQASSV VSITLIGGAG FNVGSPQQAG    660
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GVNTFIDHDL SRSHTRIGVG AEYWRDYLKL SANGYIRASG WKKSPDIEDY QERPANGWDI 240
RAEGYLPAWP QLGASLMYEQ YYGDEVGLFG KDKRQKDPHA ISAEVTYTPV PLLTLSAGHK 300
QGKSGENDTR FGLEVNYRIG EPLAKQLDTD SIRERRVLAG SRYDLVERNN NIVLEYRKSE 360
VIRIALPERI EGKGGQTLSL GLVVSKATHG LKNVQWEAPS LLAEGGKITG QGSQWQVTLP 420
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SKPETTVHNS EGITLTATAR NARGELMPGQ IITFSVTPEG ATLSNTGEVL TDQSGQAKVT 1140
LTSDKVNVYT VTAIMGKDVP VQSQVTVAVK ADAKTAHVVS VVASPDTITA DGIDSSTITS 1200
RVEDDYGFPV EGVDISHGLD TKGSPVVNIP TTRTDQSGQV TATITSTLAE TLTVNVQVPG 1260
TANQSATITL VAGTADESKS ILKSDVDTLK ADYQQSAKLT LTLQDKYGNP IVTSDHLEFV 1320
QSGPFVNFLK LSDIDYSQRN YGEYTVTVTG GKEGTATLIP MLNGVHQANL SISLNLIQSI 1380
KEMSGHVTAN NHTFSTAKFP SEGFAGAYYT LNNDNFEAGK TVDDYMFSSS QGWVSVDASG 1440
KVSFANIGDQ TSVTISAVPR QGGTTYQTLI KLKGWWVNNG NHTNIWLAAN ALCHAKNDGY 1500
NLPGITHLTS GENKRTQGSL YGEWGNVGAF SSNSQFTPGA YWTSESDDYS RHYYVQMLTG 1560
MTGSDADSSP QLTACRKSL 1579
<212> Type : PRT
<211> Length : 1579
SequenceName : SEQ ID 9
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MITHGCYTRT RHKHKLKKTL IMLSAGLGLF FYVNQNSFAN GENYFKLGSD SKLLTHDSYQ 60
NRLFYTLKTG ETVADLSKSQ DINLSTIWSL NKHLYSSESE MMKAAPGQQI ILPLKKLPFE 120
YSALPLLGSA PLVAAGGVAG HTNKLTKMSP DVTKSNMTDD KALNYAAQQA ASLGSQLQSR 180
SLNGDYAKDT ALGIAGNQAS SQLQAWLQHY GTAEVNLQSG NNFDGSSLDF LLPFYDSEKM 240
LAFGQVGARY IDSRFTANLG AGQRFFLPAN MLGYNVFIDQ DFSGDNTRLG IGGEYWRDYF 300
KSSVNGYFRM SGWHESYNKK DYDERPANGF DIRFNGYLPS YPALGAKLIY EQYYGDNVAL 360
FNSDKLQSNP GAATVGVNYT PIPLVTMGID YRHGTGNEND LLYSMQFRYQ FDKSWSQQIE 420
PQYVNELRTL SGSRYDLVQR NNNIILEYKK QDILSLNIPH DINGTEHSTQ KIQLIVKSKY 480
GLDRIVWDDS ALRSQGGQIQ HSGSQSAQDY QAILPAYVQG GSNIYKVTAR AYDRNGNSSN 540
NVQLTITVLS NGQVVDQVGV TDFTADKTSA KADNADTITY TATVKKNGVA QANVPVSFNI 600
VSGTATLGAN SAKTDANGKA TVTLKSSTPG QVVVSAKTAE MTSALNASAV IFFDQTKASI 660
TEIKADKTTA VANGKDAIKY TVKVMKNGQP VNNQSVTFST NFGMFNGKSQ TQATTGNDGR 720
ATITLTSSSA GKATVSATVS DGAEVKATEV TFFDELKIDN KVDIIGNNVR GELPNIWLQY 780
GQFKLKASGG DGTYSWYSEN TSIATVDASG KVTLNGKGSV VIKATSGDKQ TVSYTIKAPS 840
YMIKVDKQAY YADAMSICKN LLPSTQTVLS DIYDSWGAAN KYSHYSSMNS ITAWIKQTSS 900
EQRSGVSSTY NLITQNPLPG VNVNTPNVYA VCVE 934
<212> Type : PRT
<211> Length : 934
SequenceName : SEQ ID 10
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MLVLSESFKN KLLPMNGYMK GGSDSGSKAQ ARATEKGIEL QREMWQTNMQ NLAPFTPLAQ 60

QYVSQLQNLS SLQGQGQALN QYYNSQQYKD LAGQARYQSL AAAEATGGLG STATGNQLAA 120
IAPTLGQNWL SGQMNNYNNL ANIGLGALTG QANAGQNYAN NVSQLYQQQA AASAANANKP 180
SGLQSFATGA IGGAASGAMI GSAVPVIGTG IGALAGGVIG GLGSLF 226
<212> Type : PRT
<211> Length : 226
SequenceName : SEQ ID 11
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKKILSGLIL LLCCPYGFAA NGDGATHMSN LSFGPLTVAA ANNHSGYNIF EALSNTTGTY 60
PVRCHCDDTH GGPGQQTAFF PIFYTGDAAP GLVLERTLNG LNYYALNDYL SVGVTIFIIN 120
NQYAAIPFEH LSNQSTSPQH TCGAGNNGST VNLDSGRSAK LSFYVRHSIT GTVTIPTTEV 180
AWLYAGMSDH FPKTTPVSKV TIRGQLTAPQ NCELTPNQSI DVDFQKINSA EFSSTAGSII 240
AERKIKTEVT VSCTGMEDVR STEVVSASMI AANRSADATM IVTSNPDVGI KIFDKNDRPV 300
NVDGGNLPAD MGAISRLGKT DGSVTFYSAP ASLTGAKPAP DNGFTATATL VIEFTN 356

<212> Type : PRT
<211> Length : 356
SequenceName : SEQ ID 12
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MNKIYRLKWN RSRNCWSVCS ELGSRVKGKK SRAVLISAIS LYSSLVFADD VIVNQDKTID 60
FGKENQSIDY RITVTDNANL VINATDTSRP RLTLASGGGL DITGGKVTIN GPLNFLLKGT 120
GFLNVSNAGS ELYADDLYES NSGMRHDRGY FNVSNGGKIH VKGTSRLTYL QGNVSGEGSQ 180
VNSETFFMGV YGSYGGNQYL SVNNGGEVNA RKQISLGYYD QVSDTTLAVS EGGKISAPTI 240
SLSTNSELAL GAQEGSAAKA AGIIDAEKIE FVWAKTSEKK ITLNHTDKDA TISADIVSGS 300
EGLGYINALN GTTYLTGDNS AFSGKVKIEQ NGALGITQNI GTAEINNRGK LHLKADDSMT 360
FANKISGNGT ISIDSGTVEL TGNNYAFSGY IDVASGAVAV ISEDKNIGRA ELDVDGKLQI 420
NANKDWVFDN DLEGRGIVEI NMGNHEFSFD EFAYTDWFQG SLAFQNTTFN LEKNAEFLQK 480
GGITAGQGSL VTVGKGAHSI STLGFSGGTV DFGALTAGAQ MTEGTVNVSK TLDLRGEGVI 540
QVSDSDVVRS VSRDIDSALS LTEVDDGNST IKLVDAQGAE VLGDAGNLQL QDKNGQILSS 600
SAQRDIQQNG QKAAVGTYDY RLTSGVNNDG LYIGYGLTQL DLHATDSDAL VLSSNGKSEN 660
AADLSAKITG SGDLAFSSQK GQTVSLSNKD NDYTGVTDLR SGTLLLNNDN VLGNTHELRL 720
AAETELDMNG HSQTVGTLNG SADSLLSLNG GSLTVTNGGT STGSLTGSGE LNIQGGTLDI 780
AGDNSNLTAN VNIANSANVL VSHAQGLGSA NVENNGTLAL NNSAEKRAAA SVNYALGGNL 840
TNNGTLMTGM SGQQAGNVLV VKGNYHGNNG QLVMNTVLNG DDSVTDKLVV EGDTSGTTAV 900
TVNNAGGTGA KTLNGIELIH VDGKSEGEFV QAGRIVAGAY DYTLARGQGA NSGNWYLTSG 960
SDSPELQPEP DPMPNPEPNP NPEPNPNPTP TPGPDLNVDN DLRPEAGSYI ANLAAANTMF 1020
TTRLHERLGN TYYTDMVTGE QKQTTMWMRH EGGHNKWRDG SGQLKTQSNR YVLQLGGDVA 1080
QWSQNGSDRW HVGVMAGYGN SDSKTISSRT GYRAKASVNG YSTGLYATWY ADDESRNGAY 1140
LDSWAQYSWF DNTVKGDDLQ SESYKSKGFT ASLEAGYKHK LAEFNGSQGT RNEWYVQPQA 1200
QVTWMGVKAD KHRESNGTLV HSNGDGNVQT RLGVKTWLKS HHKMDDGKSR EFQPFVEVNW 1260
LHNSKDFSTS MDGVSVTQDG ARNIAEIKTG VEGQLNANLN VWGNVGVQVA DRGYNDTSAM 1320
VGIKWQF 1327
<212> Type : PRT
<211> Length : 1327
SequenceName : SEQ ID 13
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MITMKKSVLT AFITVVCATS SVMAADDNAI TDGSVTFNGK VIAPACTLVA ATKDSVVTLP 60
DVSATKLQTN GQVSGVQTDV PIELKDCDTT VTKNATFTFN GTADTTQITA FANQASSDAA 120
TNVALQMYMN DGTTAIKPDT ETGNILLQDG DQTLTFKVDY IATGKATSGN VNAVTNFHIN 180
YY 182
<212> Type : PRT
<211> Length : 182
SequenceName : SEQ ID 14

SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSKFVKTAIA ATMVMGAFAS TSTIAAGNNG TARFYGTIED SPCSIVPDDH KLEVDMGDIG 60
SGILKNNGTS TPKAFQIHLQ DCVFDTQTTM TTTFTGNASS TNSGNYYTIY NTDTGAAFNN 120
VSLAIGDAQG TSYKSGAGIE QKIVNDTATN KGKAKQTLDF KAWLVGAADA PDLGNFEANT 180
TFQITYL 187
<212> Type : PRT
<211> Length : 187
SequenceName : SEQ ID 15
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRVIFLRKEY LSLLPSMIAS LFSANGVAAA IDLCQGYDIK ASCHASRQSL SGITQVWSIA 60
DGQWLVFSDM TNNASGGAVF LQQGAEFTLS PENETGMTLF ANNTVSGEYN NGGAIFAKEN 120
STLNLTDVIF SGNVAGGYGG AIYSSGTNDT GAIDLRVTNA VFRNNIANDG KGGAIYTINN 180
DIYLSDDVFN NNQAYTSTSY SDGDGGAIDV TDNNSDSKHP SGYTIINNTA FTNNTAEGYG 240
GAIYTNSATA PYLIDISVDD SYSQNGGVLV DENNSAAGYG DGPSSAAGGF MYLGLSEVTF 300
DIADGKTLVI GNTENDGAVD SIAGTGLITK TGSGDLVLNA DNNDFTGEMQ IENGEVTLGR 360
SNSLMNVGDT HCQDDPQDCY GLTIGSIDKY QNQAELNVGS TQQTFAHSLT GFQNGTLNID 420
AGGNVTVNQG SFAGTIEGAG QLTIAQNGSY VLAGAQSMAL TGDIVVDAGA VLSLEGDAAD 480
LAALQDDPQS IVLNGGMLDL SDFSTWQSGT SYKDGLEVSG SSGTVIGSQD VVDLAGGNDM 540
HIGGDGKDGV YVVIDAGDGQ VSLANDNQYL GTTQIASGTL MVSDNSQLGY THYNRQVIFT 600
DKPQESVMEI TANVDTRSTT TEHGRDIEMR ADGEVAVDAG VDTQWGALMA DSSGQHQDEG 660
STLTKTGAGT LELTASGTTQ SAVRVEEGTL QGDVADIFPY ASSLWVGDGA TFVTGADQDI 720
QSIDATSSGT IDISDGTVLR LTGQDTSVAL NASLFNCDGT LVNATDGVTL TGELNTNLET 780
DSLTYLSNVT VNGNLTNTSG AVSLQNGVAG DTLTVNGDYT GGGTLLLDSE LNGDDSVSDQ 840
LVMNGNTAGN TTVVVNSITG IGEPTSTGIK VVDFAADPTQ FQNNAQFSLA GSGYVNMGAY 900
DYTLVEDNND WYLRSQEVTP PSPPDPDPTP DPDPTQDPDP TPDPEPTPAY QPVLNAKVGG 960
YLNNLRAANQ AFMMERRDHA GGDGQTLNLR VIGGDYHYTA AGQLAQHEDT STVQLSGDLF 1020
SGRWGTDGEW MLGIVGGYSD NQGDSRSSMT GTRADNQNHG YAVGLTSSWF QHGKQKQGAW 1080
LDNWLQYAWF SNDVSÉHEDG VDHYHSSGII ASLEAGYQWL PGRGVVIEPQ AQVIYQGVQQ 1140
DDFTAANRAR VSQSQGDDIQ TRLGLHSEWR TAVHVIPTLD LNYYHDPHST EIEEDASTIS 1200
DDAVKQRGEI KVGVTGNISQ RVSLRGSVAW QKGSDDFAQT AGFLSMTVKW 1250
<212> Type : PRT
<211> Length : 1250
SequenceName : SEQ ID 16
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MHSWKKKLIV SQLALACTLA ITSQANAATN DISGQTYNTF HHYNDATYAD DVYYDGYVGW 60
NNYAADSYYN GDIYPVINNA TVNGVISTYY LDDGISTNTN ANSLTIKNST IHGMITSECM 120
TTDCADDRAT GYVYDRLTLS VDNSTIDDNY EHYTYNGTYN NAADTHVVDV YDMGTAITLD 180
QEVDLSITNN SHVAGITLTQ GYEWEDIDDN TVSTGVNSSE VFNNTITVKD STVTSGSWTD 240
EGTTGWFGHT GNASNYSNTL TADDVAIAAI ANPYADNAMQ TTVTLDNSTL MGDVVFSSNF 300
DENFFPQGAN SYRDADGDVD TNGWDGTDRM DVTLNNGSKW VGAAMSVHMV DEDGDGSYDG 360
YAVGTEATAT LLDIAANSLW PSSTVGVDNI NTQYDENGHI VGNEVYQSGL FNVTLNGGSE 420
WDTTKSSLID TLSINSGSQV NVADSRLISD TVSLTGGSNL NIGEDGHVAT NTLTIDNSTV 480
KMSDDVSAGW GLEDAALYAN TITVTNDGLL DINVDQFDAN PFQADTLNLT STTDTNGNIH 540
AGVFDIHSSD YVMDTDLVND RTNDTTKSNY GYGLIAMNSD GHLTINGNGD NDNTASIEAG 600
QNEVDNNGDH VAAATGNYKV RIDNATGAGS IADYNGNELI YVNDKNSNAT FSAANKADLG 660
AYTYQAEQRG NTVVLQQMEL TDYANMALSI PSANTNIWNL EQDTVGTRLT NSRHGLADNG 720
GAWVSYFGGN FNGDNGTINY DQDVNGIMVG VDTKIDGNNA KWIVGAAAGF AKGDMNDRSG 780
QVDQDSQTAY IYSSAHFANN VFVDGSLSYS HFNNDLSATM SNGTYVDGST NSDAWGFGLK 840
AGYDFKLGDA GYVTPYGSIS GLFQSGDDYQ LSNDMKVDGQ SYDSMRYELG VDAGYTFTYS 900
EDQALTPYFK LAYVYDDSNN DNDVNGDSID NGTEGSAVRV GLGTQFSFTK NFSAYTDANY 960
LGGGDVDQDW SANVGVKYTW 980
<212> Type : PRT

<211> Length : 980
SequenceName : SEQ ID 17
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKLKHVGMIV VSVLAMSSAA VSAAEGDESV TTTVNGGVIH FKGEVVNAAC AIDSESMNQT 60
VELGQVRSSR LAKAGDLSSA VGFNIKLNDC DTNVSSNAAV AFLGTTVTSN DDTLALQSSA 120
AGSAQNVGIQ ILDRTGEVLI LDGATFSAKT DLIDGTNILP FQARYIALGQ SVAGTANADA 180
TFKVQYL 187
<212> Type : PRT
<211> Length : 187
SequenceName : SEQ ID 18
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKLLKVAAIA AIVFSGSALA GVVPQYGGGG GNHGGGGNNS GPNSELNIYQ YGGGNSALAL 60
QADARNSDLT ITQHGGGNGA DVGQGSDDSS IDLTQRGFGN SATLDQWNGK DSHMTVKQFG 120
GGNGAAVDQT ASNSTVNVTQ VGFGNNATAH QY 152
<212> Type : PRT
<211> Length : 152
SequenceName : SEQ ID 19
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MPIGNLGHNP NVNNSIPPAP PLPSQTDGAG GRGQLINSTG PLGSRALFTP VRNSMADSGD 60
NRASDVPGLP VNPMRLAASE ITLNDGFEVL HDHGPLDTLN RQIGSSVFRV ETQEDGKHIA 120
VGQRNGVETS VVLSDQEYAR LQSIDPEGKD KFVFTGGRGG AGHAMVTVAS DITEARQRIL 180
ELLEPKGTGE SKGAGESKGV GELRESNSGA ENTTETQTST STSSLRSDPK LWLALGTVAT 240
GLIGLAATGI VQALALTPEP DSPTTTDPDA AASATETATR DQLTKEAFQN PDNQKVNIDE 300
LGNAIPSGVL KDDVVANIEE QAKAAGEEAK QQAIENNAQA QKKYDEQQAK RQEELKVSSG 360
AGYGLSGALI LGGGIGVAVT AALHRKNQPV EQTTTTTTTT TTTSARTVEN KPANNTPAQG 420
NVDTPGSEDT MESRRSSMAS TSSTFFDTSS IGTVQNPYAD VKTSLHDSQV PTSNSNTSVQ 480
NMGNTDSVVY STIQHPPRDT TDNGARLLGN PSAGIQSTYA RLALSGGLRH DMGGLTGGSN 540
SAVNTSNNPP APGSHRFV 558
<212> Type : PRT
<211> Length : 558
SequenceName : SEQ ID 20
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MFSTFKKAAL LAAIALPFST MAAPTVTFQG EVTDQTCSVN INGQTNSVVL MPTVAMADFG 60
ATLADGQSAG QTPFTVSVSN CQAPTGADQA INTTFLGYDV DASTGVMGNR DTSSDAAKGF 120
GIQLMDSSTS GNPVTLAGAT NVPGLTLKVG DTEASYDFGA RYFVIDSAAA TAGKITAVAE 180
YTLSYL 186
<212> Type : PRT
<211> Length : 186
SequenceName : SEQ ID 21
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MNSEGGKPGN VLTVNGNYTG NNGLMTFNAT LGGDNSPTDK MNVKGDTQGN TRVRVDNIGG 60
VGAQTVNGIE LIEVGGNSAG NFALTTGTVE AGAYVYTLAK GKGNDEKNWY LTSKWDGVTP 120

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ADTPDPINNP PVVDPEGPSV YRPEAGSYIS NIAAANSLFS HRLHDRLGEP QYTDSLHSQD   180
SASSMWMRHV GGHERSSAGD GQLNTQANRY VLQLGGDLAQ WSSNAQDRWH LGVMAGYANQ   240
HSNTQSNRVG YKSDGRISGY SAGLYATWYQ NDANKTGAYV DSWALYNWFD NSVSSDNRSA   300
DDYDSRGVTA SVEGGYTFEA GTCSGSEGTL NTWYVQPQAQ ITWMGVKDSD HARKDGTRIE   360
TEGDGNVQTR LGVKTYLNSH HQRDDGKQRE FQPYIEANWI NNSKVYAVKM NGQTVSRDGA   420
RNLGEVRTGV EAKVNNNLSL WGNVGVQLGD KGYSDTQGML GVKYSW                  466
<212> Type : PRT
<211> Length : 466
      SequenceName : SEQ ID 22
      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSYLNLRLYQ RNTQCLHIRK HRLAGFFVRL FVACAFAVQA PLSSAELYFN PRFLADDPQA    60
VADLSRFENG QELPPGTYRV DIYLNNGYMA TRDVTFNTGD SEQGIVPCLT RAQLASMGLN   120
TASVAGMNLL ADDACVPLTT MVQDATAHLD VGQQRLNLTI PQAFMSNRAR GYIPPELWDP   180
GINAGLLNYN FSGNSVQNRI GGNSHYAYLN LQSGLNIGAW RLRDNTTWSY NSSDRSSGSK   240
NKWQHINTWL ERDIIPLRSR LTLGDGYTQG DIFDGINFRG AQLASDDNML PDSQRGFAPV   300
IHGIARGTAQ VTIKQNGYDI YNSTVPPGPF TINDIYAAGN SGDLQVTIKE ADGSTQIFTV   360
PYSSVPLLQR EGHTRYSITA GEYRSGNAQQ EKPRFFQSTL LHGLPAGWTI YGGTQLADRY   420
RAFNFGIGKN MGALGALSVD MTQANSTLPD DSQHDGQSVR FLYNKSLNES GTNIQLVGYR   480
YSTSGYFNFA DTTYSRMNGY NIETQDGVIQ VKPKFTDYYN LAYNKRGKLQ LTVTQQLGRS   540
STLYLSGSHQ TYWGTSNVDE QFQAGLNTAF EDINWTLSYS LTKNAWQKGR DQMLARNVNI   600
PFSHWLRSDS KSQWRHASAS YSMSHDLNGR MTNLAGVYGT LLEDNNLSYS VQTGYAGGGD   660
GNSGSTGYAT LNYRGGYGNA NIGYSHSDDI KQLYYGVSGG VLAHANGVTL GQPLNDTVVL   720
VKAPGAKDAK VENQTGVRTD WRGYAVLPYA TEYRENRVAL DTNTLADNVD LDNAVANVVP   780
TRGAIVRAEF KARVGIKLLM TLTHNNKPLP FGAMVTSESS QSSGIVADNG QVYLSGMPLA   840
GKVQVKWGEE ENAHCVANYQ LPPESQQQLL TQLSAECR                          878
<212> Type : PRT
<211> Length : 878
      SequenceName : SEQ ID 23
      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MQIIFGEKCV SLLRLFFAAV LMLWCAQTAA YSGQCHTTQG NPYIGVNFGV KTLEEEENTT    60
GVVKDKFYQW NESNDYYVSC DCDKDNVRSG RWAFAADSPL VYLGDNWYKI NDYLAAKVLL   120
QVKGSSPTAV PFENVGTGAD TRWHICDPGG QRLGGQGASG NSGSFSLKIL QPFVGSVVIP   180
PMALARLFEC YNIPAGDSCT TTGTPVLVYY LSGTINSLGS CSVNAGETIE VDLGDVFAAN   240
FRVVGHKPLG ARTAELAIPV RCNTGNAGLV NVNLSLTATT DPSYPQAIKT SRPGVGVVVT   300
DSQNNIISPA GGTLPLSIPD DADSIA                                       326
<212> Type : PRT
<211> Length : 326
      SequenceName : SEQ ID 24
      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKIKTLAIVV LSALSLSSTA ALAAATTVNG GTVHFKGEVV NAACAVDAGS VDQTVQLGQV    60
RTASLAQDGA TSSAVGFNIQ LNDCDTNVAS KAAVAFLGTV IDAGHTNVLA LQSSAAGSAT   120
NVGVQILDRT GAALTLDGAT FSEQTTLNNG TNTIPFQARY YAIGEATPGA ANADATFKVQ   180
YQ                                                                 182
<212> Type : PRT
<211> Length : 182
      SequenceName : SEQ ID 25
      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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MKLKVIATLI ATVAVGVSFN SNFASASTTS ASLTVNSNLT MGTCSAQIMD NSNKVINEVV 60
FGNVYISELG AKSKVQQFKI RFSNCSGLPQ NSAQIVLAPN GISCAGSQSS SAGFSNKFTD 120
ASAATRTAVE VWTTDTPESN GSTQFHCAQK IPVPVTLPAD TTTQPYDYPL SARMTVAEGR 180
LVTDVRPGNF RSPTTFTITY Q 201
<212> Type : PRT
<211> Length : 201
SequenceName : SEQ ID 26
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MASTVEYGET VDGVVLEKDI QLVYGTANNT KINPGGEQHI KEFGISSNTE INGGYQYIEM 60
NGTAEYSVLN DGYQIVQMGG AANQTTLNNG VLQVYGAAND PTIKGGRLIV EKDGITVLAA 120
IEKGGLLEVK EGGLAIAVDQ KAGGAIKAST RVMEVFGTNR LGQFEIKNGI ANNMLLENGG 180
SLRVEENDFA YNTTVDSGGL LEVMDGGTAT GVDKKAGGKL IVSTNALEVS GTNSKGQFSI 240
KDGVSKNYEL DDGSGLIVME DTQAIDTILD EHATMQSLGK DTGTRVQANA VYDLGRSDQN 300
GSITYSSKAI SENMVINNGR ANVWAGTMVN VSVRGNDGIL EVMKPQINYA PAMLVGKVVV 360
SEGASLRTHG AVDTSKADVS LENSAWTIIA DITTTNQNTR LNLANLAMSG ANVIMMDESV 420
TRSSVTASAE NFTTLTTNTL SGNGNFYMRT DMANHQSDQL NVTGQATGDF KIFVTDTGAS 480
PAAGDSLTLV TTGGGDAAFT LGNAGGVVDI GTYEYTLLDN GNHSWSLAEN RAQITPSTTD 540
VLNMAAAQPL VFDAELDTVR ERLGSVKGVS YDTAMWSSAI NTRNNVTTDA GAGFEQTLTG 600
LTLGIDSRFS REESSTIRGL FFGYSHSDIG FDRGGKGNVD SYTLGAYAGW EHQNGAYVDG 660
VVKVDRFANT IHGKMSNGAT AFGDYNSNGA GAHVESGFRW VDGLWSVRPY LAFTGFTTDG 720
QDYTLSNGMR ADVGNTRILR AEAGTAVSYH MDLQNGTTLE PWLKAAVRQE YADSNQVKVN 780
DDGKFNNDVA GTRGVYQAGI RSSFTPTLSG HLSVSYGNGA GVESPWNTQA GVVWTF 836

<212> Type : PRT
<211> Length : 836
SequenceName : SEQ ID 27
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MQRKGNKLLI QLCSVILLFF TTSWYALANE CYIERNAEGD YHMKISSTQL SLASQMVEVP 60
TEIAEATWDV NIQLRGDAIG CKSLGDSKAV HFLNTADPSL ISTYTTTNGA ALLKTTVPGI 120
VYSVELLCLS CGAADELDLW LPAQSGADNF IPSTQTKWAY EYSDQSWYLR FRLFITPEFK 180
PKNGVSSGTT IAGKIASWYI GTNDQPWINF YIDNDSLKFF VDEPTCATVA LAQDQGNVSG 240
NQVTLGNSYV SEVKNGLTRE IPFSIRAEYC YASKITVKLK AANKPSDATL VGKTTGSASG 300
VAVKVNSTYD NSKVLLKADG SNTVDYNFAA WSNNLLFLPF TAQLVPDGSG NAVGVGTFSG 360
NATFSFTYE 369
<212> Type : PRT
<211> Length : 369
SequenceName : SEQ ID 28
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MYQFTHQKSR IPKKTLLAAC CALFYSSNGA AADTVEYDSS FLMGTGASTI DVKRYAQGNP 60
TPPGLYNVRV FVNGQATSSL EIPFVDIGEN SAAACLTHKN LAQLHIKQPE QPVTLLAREG 120
EEEDCLDLAK SYEKADVCFD GSDQFLDLTI PQAYVLKSYG GYVDPSLWES GINAATLAYT 180
LNAYHTSSDN DNSDSVYGAF NSGINLGAWH FRARGNYNWT TDNGSDFDFQ DRYLQRDIPA 240
IRSQIIMGDA YTTGETFDSV NVRGVRLYSD SRMLPSALAS YAPTIRGVAN SNAKVTVTQS 300
GYKIYETTVP PGEFVIDDIS PSGFGSELVV TIEEADGSKR TFTQPFSSVV QMQRPGVGRW 360
DFSAGKVIDD SLRSEPNMGQ ASYYYGLNNL FTGYTGIQFT DNNYLAGLLG VGINTSIGAF 420
AVDVTHSRAE IPDDKTYQGQ SYRVTWNKLF QDTGTSFNLA AYRYSTQDYL GLHDALVLID 480
DAKHLSADED KNTMQTYSRM KNQFTVSINQ PLNIAYEDYG SLFISGSWTY YWAANNSRTE 540
YNVGYSKSVS WGSFSVNLQR SWNEDGEKDD AMYVSVSVPI ENILGGKRKS SGFRNLNTQL 600
NTDFDGSHQL NVNSSGNTEN NLVNYSVNAG YSLDKNAGDL ASVGGYLNYE SGLGGISASA 660
SATSDNSQQY SISTDGGFVL HSGGLTFTNN SFSSNDTLVL INALGAKGAR INNSNNEIDR 720
WGYAVTSSVS PYRENRVGLN IETLENDVEL KSTSATTVPR SGSVVLTRFE TDEGRSAVLN 780
ITAANGKSIP FAAEVYQGEV MIGSMGQGGQ AFVRGINDSG ELIVRWYENN QTIDCKLHYQ 840

FPAQPQTQGS TNTLLLNNLT CQVANH 866
<212> Type : PRT
<211> Length : 866
SequenceName : SEQ ID 29
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKFKRLLHSG IASLSLVACG VNAATDLGPA GDIHFSITIT TKACEMEKSD LEVDMGTMTL 60
QKPAAVGTVL SKKDFTIELK ECDGISKATV EMDSQSDSDD DSMFALEAGG ATGVALKIED 120
DKGTQQVPKG SSGTPIEWAI DGETTSLHYQ ASYVVVNTQA TGGTANALVN FSITYE 176

<212> Type : PRT
<211> Length : 176
SequenceName : SEQ ID 30
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKYNNIIFLG LCLGLTTYSA LSADSVIKIS GRVLDYGCTV SSDSLNFTVD LQKNSARQFP 60
TTGSTSPAVP FQITLSECSK GTTGVRVAFN GIEDAENNTL LKLDEGSNTA SGLGIEILDG 120
NMRPVKLNDL HAGMQWIPLV PEQNNILPYS ARLKSTQKSV NPGLVRASAT FTLEFQ 176

<212> Type : PRT
<211> Length : 176
SequenceName : SEQ ID 31
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKWRKRGYLL AAILALASAT IQAADVTITV NGKVVAKPCT VSTTNATVDL GDLYSFSLMS 60
AGAASAWHDV ALELTNCPVG TSRVTASFSG AADSTGYYKN QGTAQNIQLE LQDDSGNTLN 120
TGATKTVQVD DSSQSAHFPL QVRALTVNGG ATQGTIQAVI SITYTYS 167
<212> Type : PRT
<211> Length : 167
SequenceName : SEQ ID 32
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKRAPLITGL LLISTSCAYA SSEGCGADST SGATNYSSVV DDVTVNQTDN VTGREFTSAT 60
LSSTNWQYAC SCSAGKAVKL VYMVSPVLTT TGHQTGYYKL NDSLDIKTMN RPGNPGD 117

<212> Type : PRT
<211> Length : 117
SequenceName : SEQ ID 33
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKKALLAAAL VMASGSALAV DGGHIDFNGM VQSGTCKVGV VDTGMHSVTT DGVVTLDTAN 60
VTDTFAEVSA TAVGLLPKEF MISVECDPGA PKNAELTMGS ASYANTSGTL NNNMNITVNG 120
IAPAQNVNIA VHNMKNKAGA AEIKQVHMNN SSEVQELTLD AEGKGQYVFN ASYVKAPNSP 180
AVTAGHVTTN ALYTVAYK 198
<212> Type : PRT
<211> Length : 198
SequenceName : SEQ ID 34

SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKPNMIVGAL ALTSVFMAGH LQAADGTVHF RGEIIDSTCE VTPETKDQVV DLGKVNRTAF 60
SGVDDVAAPT AFSIDLTQCP ETFKSAAIRF DGNEDAHGNG NLAIGTPLDN SNDAAAGISP 120
SDNSGDYTGA GAVSAAKGVA IRLYNRADNT QVKLYENSAS TPISNGNASM KFMARYIATE 180
TTIDPGTANA DSQFTVEYIK 200
<212> Type : PRT
<211> Length : 200
SequenceName : SEQ ID 35
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MPIFQREGHL KYSFAAGEYQ AGNYDSASPR FGQLDLIYGL PWGMTAYGGV LISNNYNAFT 60
LGIGKNFGYI GAISIDVTQA KSELNNDRDS QGQSYRFLYS KSFESGTDFR LAGYRYSTSG 120
FYTFQEATDV RSDADSDYNR YHKRSEIQGN LTQQLGAYGS VYLNLTQQDY WNDAGKQNTV 180
SAGYNGRIGK VSYSIAYSWN KSPEWDESDR LWSFNISVPL GRAWSNYRVT TDQDGRTNQQ 240
VGVSGTLLED RNLSYSVQEG YASNGVGNSG NANVGYQGGS GNVNVGYSYG KDYRQLNYSV 300
RGGVIVHSEG VTLSQPLGET MTLISVPGAR NARVVNNGGV QVDWMGNAIV PYAMPYRENE 360
ISLRSDSLGD DVDVENAFQK VVPTRGAIVR ARFDTRVGYR VLMTLLRSAG SPVPFGATAT 420
LITDKQNEVS SIVGEEGQLY ISGMPEEGRV LIKWGNDASQ QCVAPYKLSL ELKQGGIIPV 480
SANCQ 485
<212> Type : PRT
<211> Length : 485
SequenceName : SEQ ID 36
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSGYTVKPPT GDSNEQTQFI DYFNLFYSKR DQEQISISQQ LGNYGATFFS ASRQSYWNTS 60
RSDQQISFGL NVPFGDITTS LNYSYSNNIW QNDRDHLLAF TLNVPFSHWM RTDSQSAFRN 120
SNASYSMSND LKGGMTNLSG VYGTLLPDNN LNYSVQVGNT HGGNTSSGTS GYSTLNYRGA 180
YGNTNVGYSR SGDSSQIYYG MSGGIIAHAD GITFGQPLGD TMVLVKAPGA DNVKIENQTG 240
IHTDWRGYAI LPFATEYREN RVALNANSLA DNVELDETVV TVIPTHGAIA RATFNAQIGG 300
KVLMTLKYGN KSVPFGAIVT HGENKNGSIV AENGQVYLTG LPQSGKLQVS WGNDKNSNCI 360
VDYKLPEVSP GTLLNQQTAI CR 382
<212> Type : PRT
<211> Length : 382
SequenceName : SEQ ID 37
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSALYERSQL TQVMISSAPA TAETMEKAEY LRLDCTIKEV QFTAGQKQDI DVTTLCSTEQ 60
ENINGLGASS EISMSGNFYL NQAQNALRDA YDNDTVYAFK VQFPSGKGFK FLAEVRQHTW 120
SSGTNGVVAA TFSLRLKGKP VSYVVPLAFV KNLDKTLTVN TGALLTMSVS VNGGTPPYKH 180
AWKKDGQPVE GQTTDTFSKP GAQSGDKGAY TCEVTDSAEQ PQSITSDACT VTVNGAGG 238

<212> Type : PRT
<211> Length : 238
SequenceName : SEQ ID 38
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

MRNKPFYLLC AFLWLAVSHA LAADSTITIR GYVRDNGCSV AAESTNFTVD LMENAAKQFN 60
NIGATTPVVP FRILLSPCGN AVSAVKVGFT GVADSHNANL LALENTVSAA SGLGIQLLNE 120
QQNQIPLNAP SSAISWTTLT PGKPNTLNFY ARLMATQVPV TAGHINATAT FTLEYQ 176

<212> Type : PRT
<211> Length : 176
SequenceName : SEQ ID 39
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MNKSVVSISA AMLVLLCQPV MGSEISPATP SDEDNYTFDP QLFRGSRFSQ SSLAKLTTRE 60
SVAPGNYKMD IYTNNKLSGS WNVTFKEAAD GRVLPCLTPE VADAIGLKTG EDKGEKDPVC 120
TFAKELAPGI TSQTQLSQLR LDLSVPQSQL ISRPRGYVPP SELDTGASLA FMNYIANYYN 180
VAYSGQNAHS QRSLWASFNG GINLGAWQYR QLSNMTWDND KGNQWNNIRS YLQRPLPAIN 240
SQLMMGQLIT SGRFFSGLSY HGVSLATDER MLPDSMRGYA PTIRGVAATN ARVSVMQNGH 300
EIYQTTVAPG PFEINDLYPT SYSGDLDVTV TEANGAVSRF SVPFSAVPES MRPGTSRYNV 360
EVGKTQDSGD DSMFGDLTWQ HGMTNTLTFN SGSRIADGYQ ALMLGGVYGS SLGAFGANLT 420
WSHARVPESE AQSGWMSQLT WSKTFQPTST TVSLAGYRYS TSGYRDLADV LGERHAASNK 480
QSWDSSQWRQ QSRFDLTLSQ SLANYGNLFV SGSTQNYRGG KSRDTQLQLG YSNSFSHGIS 540
MNLSVGRQRM GGYKDNSDDM QTVTSLSFSF PLGGNGPRVP SLSNSWTHST DGSSQLQSSL 600
TGMLDEAQTT NYSLNVMRDQ QYKQTTLSGN MQKRFSQTTV GLNASKGQDY WQASGNVQGA 660
MAVHGGGITF GPYLGETFAL VEAKGAEGAK VYNSSQLEIN DSGYALVPAV TPYRYNRISL 720
DPQGMDGDAE LVDSERQVAP VAGAAVKVIF RTRPGKALLI KSRMADGSEL PMGADVLDEN 780
NTVVGIAGQG GQIYLRTEQT KGHLSVRWGE GANDSCQLPF DISGKDSNSP IIRLNETCQS 840

<212> Type : PRT
<211> Length : 840
SequenceName : SEQ ID 40
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKLAACFLTL LPGFAVAASW TSPGFPAFSE QGTGTFVSHA QLPKGTRPLT LNFDQQCWQP 60
ADAIKLNQML SLQPCSNTPP QWRLFRDGKY TLQIDTRSGT PTLMISIQNA AEPVANLVRE 120
CPKWDGLPLT LDVSATFPEG AAVRDYYSQQ IAIVKNGQIT LQPAATSNGL LLLERAETDA 180
SAPFDWHNAT VYFVLTDRFE NGDPSNDQSY GRHKDGMAEI GTFHGGDLRG LTNKLDYLQQ 240
LGVNALWISA PFEQIHGWVG GGTKGDFPHY AYHGYYTQDW TNLDANMGNE ADLRTLVDSA 300
HQRGIRILFD VVMNHTGYAT LADMQEYQFG ALYLSGDEVK KTLGERWSDW KPAAGQTWHS 360
FNDYINFSDK TGWDKWWGKN WIRTDIGDYD NPGFDDLTMS LAFLPDIKTE STTASGLPVF 420
YKNKTDTHAK AIDGFTPRDY LTHWLSQWVR DYGIDGFRVD TAKHVELPAW QQLKTEASAA 480
LREWKKANPD KALDDKPFWM TGEAWGHGVM QSDYYRHGFD AMINFDYQEQ AAKAVDCIAQ 540
MDTTWQQMAE KLQGFNVLSY LSSHDTRLFR EGGDKAAELL LLAPGAVQIF YGDESSRPFG 600
PTGSDPLQGT RSDMNWQDVS GKSAANVAHW QKISQFRARH PAIGAGKQTT LSLKQGYGFV 660
REHGDDKVLV IWAGQQ 676
<212> Type : PRT
<211> Length : 676
SequenceName : SEQ ID 41
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MPQRHHQGHK RTPKQLALII KRCLPMVLTG SGMLCTTANA EEYYFDPIML ETTKSGMQTT 60
DLSRFSKKYA QLPGTYQVDI WLNKKKVSQK KITFTANAEQ LLQPQFTVEQ LRELGIKVDE 120
IPALAEKDDD SVINSLEQII PGTAAEFDFN HQRLNLSIPQ IALYRDARGY VSPSRWDDGI 180
PTLFTNYSFT GSDNRYRQGN RSQRQYLNMQ NGANFGPWRL RNYSTWTRND QASSWNTISS 240
YLQRDIKALK SQLLLGESAT SGSIFSSYNF TGVQLASDDN MLPNSQRGFA PTVRGIANSS 300
AIVTIRQNGY VIYQSNVPAG AFEINDLYPS SNSGDLEVTI EESDGTQRRF IQPYSSLPMM 360
QRPGHLKYSA TAGRYRADAN SDSKEPEFAE ATAIYGLNNT FTLYGGLLGS EDYYALGIGI 420
GGTLGALGAL SMDINRADTQ FDNQHSFHGY QWRTQYIKDI PETNTNIAVS YYRYTNDGYF 480
SFDEANTRNW DYNSRQKSEI QFNISQTIFD GVSLYASGSQ QDYWGNNEKN RNISVGVSGQ 540

QWGIGYSLNY QYSRYTDQNN DRALSLNLSI PLERWLPRSR VSYQMTSQKD RPTQHEMRLD 600
GSLLDDGRLS YSLEQSLDDD NNHNSSVNAS YRSPYGTFSA GYSYGNDSSQ YNYGVTGGVV 660
IHPHGVTLSQ YLGNAFALID ANGASGVRIQ NYPGIATDPF GYAVVPYLTT YQENRLSVDT 720
TQLPDNVDLE QTTQFVVPNR GAMVAARFNA NIGYRVLVTV SDRNGKPLPF GALASNDDTG 780
QQSIVDEGGI LYLSGISSKS QSWTVRWGNQ ADQQCQFAFS TPDSEPTTSV LQGTAQCH 838

<212> Type : PRT
<211> Length : 838
SequenceName : SEQ ID 42
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MMFRNRILLI FILWANFTWA GCRTTASLNI TDGINVGEIL ANETSFSKSV VFTGISCDTS 60
TDKIVYKNIQ SDWVEVGPFG NGEKLKVKIE SLGKTSDTIG KSSNAQAVLP YVVKIARGTP 120
DFTGERKSTW FISDTVIANI GGESSSSIDF WLGICKALKF NWCVNYLTSK LAGDTFTLGL 180
NISYYPKNTT CKPENTVIKV DDIALFQLRN QGKIAANSKE GTITLKCDNL FGDKKQASRN 240
MVVYLSSSDL VKGSNTILRG KTDNGVGFVL DLTEPPKGTE AAIKISANGD QGAATSLWKT 300
DKPGVSLNSN IINIPVMASY YVYDEKKVKS GALEATALIN VKYD 344
<212> Type : PRT
<211> Length : 344
SequenceName : SEQ ID 43
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MIKKASLLTA CSVTAFSAWA QDTSPDTLVV TANRFEQPRS TVLAPTTVVT RQDIDRWQST 60
SVNDVLRRLP GVDITQNGGS GQLSSIFIRG TNASHVLVLI DGVRLNLAGG SGSADLSQFP 120
IALVQRVEYI RGPRSAVYGS DAIGGVVNII TTRDEPGTEI SAGWGSNSYQ NYDVSTQQQL 180
GDKTRVTLLG DYAHTHGYDV VAYGNTGTQA QPDNDGFLSK TLYGALEHNF TDAWSGFVRG 240
YGYDNRTNYD AYYSPGSPLV DTRKLYSQSW DAGLRYNGEL IKSQLITSYS HSKDYNYDPH 300
YGRYDSSATL DEMKQYTVQW ANNIIIGHGN VGAGVDWQKQ STAPGTAYVK DGYDQRNTGI 360
YLTGLQQVGD FTFEGAARSD DNSQFGRHGT WQTSAGWEFI EGYRFIASYG TSYKAPNLGQ 420
LYGFYGNPNL DPEKSKQWEG AFEGLTAGVN WRISGYRNDV SDLIDYDDHT LKYYNEGKAR 480
IKGVEATANF DTGPLTHTVS YDYVDARNAI TDTPLLRRAK QQVKYQLDWQ LYDFDWGITY 540
QYLGTRYDKD YSSYPYQTVK MGGVSLWDLA VAYPVTSHLT VRGKIANLFD KDYETVYGYQ 600
TAGREYTLSG SYTF 614
<212> Type : PRT
<211> Length : 614
SequenceName : SEQ ID 44
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKNKLLFMML TILGAPGIAA AAGYDLANSE YNFAVNELSK SSFNQAAIIG QAGTNNSAQL 60
RQGGSKLLAV VAQEGSSNRA KIDQTGDYNL AYIDQAGSAN DASISQGAYG NTAMIIQKGS 120
GNKANITQYG TQKTAIVVQR QSQMAIRVTQ R 151
<212> Type : PRT
<211> Length : 151
SequenceName : SEQ ID 45
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MNIFAYLLVL VFSMSMSSSA FASVVMTGTR IIFPGDAKEK TIQLRNTSDQ PYIINIHVED 60
ERGSDKNVPF MPTPQTFRME AAAGQALRLL YTGNNLPQDR ESVFWFSFSQ LPYLNKNDKS 120
QNQLILALTN RVKIFYRPSS IVGKSSDAPK NLTYQVKQNR IEVTNPTGYY VTIRAAELLN 180
NGKKVPLANS VMIAPQSTTE WTLPSGISVA PGAQIHLVTV NDYGVNVTSE HAL 233

<212> Type : PRT
<211> Length : 233
SequenceName : SEQ ID 46
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKRLHKRFLL ATFCALLTAT LQAADVTITV NGRVVAKPCT IQTKEANVNL GDLYTRNLQQ 60
PGSASGWHNI TLSLTDCPAE TSAVTAIVTG STDNTGYYKN EGTAENIQIE LRDDQDATLK 120
NGDSKTVIVD EITRNAQFPL KARAITVNGN ASQGTIEALI NVIYTWQ 167
<212> Type : PRT
<211> Length : 167
SequenceName : SEQ ID 47
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRAKLLGIVL TTPIAISSFA STETLSFTPD NINADISLGT LSGKTKERVY LAEEGGRKVS 60
QLDWKFNNAA IIKGAINWDL MPQISIGAAG WTTLGSRGGN MVDQDWMDSS NPGTWTDESR 120
HPDTQLNYAN EFDLNIKGWL LNEPNYRLGL MAGYQESRYS FTARGGSYIY SSEEGFRDDI 180
GSFPNGERAI GYKQRFKMPY IGLTGSYRYE DFELGGTFKY SGWVEASDND EHYDPGKRIT 240
YRSKVKDQNY YSVSVNAGYY VTPNAKVYVE GTWNRVTNKK GNTSLYDHND NTSDYSKNGA 300
GIENYNFITT AGLKYTF 317
<212> Type : PRT
<211> Length : 317
SequenceName : SEQ ID 48
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MFFKRGKILS AGRLNKKSLG IVMLLSVGLL LAGCSGSKSS DTGTYSGSVY TVKRGDTLYR 60
ISRTTGTSVK ELARLNGISP PYTIEVGQKL KLGGAKSSSS TRKSTAKSTT KTASVTPSSA 120
VPKSSWPPVG QRCWLWPTTG KVIMPYSTAD GGNKGIDISA PRGTPIYAAG AGKVVYVGNQ 180
LRGYGNLIMI KHSEDYITAY AHNDTMLVNN GQSVKAGQKI ATMGSTDAAS VRLHFQIRYR 240
ATAIDPLRYL PPQGSKPKC 259
<212> Type : PRT
<211> Length : 259
SequenceName : SEQ ID 49
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MPTPNPLAPV KGAGTTLWVY NGNGDPYANP LSDNDWSRLA KVKDLTPGEL TAESYDDSYL 60
DDEDADWAAT GQGQKSAGDT SFTLAWMPGE QGQQALLAWF NEGDTRAYKI RFPNGTVDVF 120
RGWVSSIGKA VTAKEVITRT VKVTNVGRPS MAEDRSTVTA ATGMTVTPAS TSVVKGQSTT 180
LTVAFQPEGA TDKSFRAVSA DKTKATVSVS GMTITVKGVA AGKVNIPVVS GNGEFAAVAE 240
INVTAS 246
<212> Type : PRT
<211> Length : 246
SequenceName : SEQ ID 50
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSALYERSQL TQVMISSAPA TAETMDKAEY LRLDCTIKEV QFTAGQKQDI DVTTLCSTEQ 60
ENINGLGASS EISMSGNFYL NQAQNALRDA YDNDALYAFK VLFPSGKGFK FLAEVRQHTW 120
SSGTNGVVAA TFSLRLKGKP VSFVVPLAFV KNLDKTLTVN TGALLTMSVS ANGGTPPYKY 180

AWKKDGQPVD GQTTDTFSKP GAQSADAGKY TCVVTDSAEK AQSVTSVECT VTVSAAAG 238

<212> Type : PRT
<211> Length : 238
SequenceName : SEQ ID 51
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKKSTLALVV MGIVASASVQ AAEIYNKDGN KLDVYGKVKA MHYMSDNDSK DGDQSYIRFG 60
FKGETQINDQ LTGYGRWEAE FAGNKAESDT AQQKTRLAFA GLKYKDLGSF DYGRNLGALY 120
DVEAWTDMFP EFGGDSSAQT DNFMTKRASG LATYRNTDFF GVIDGLNLTL QYQGKNENRD 180
VKKQNGDGFG TSLTYDFGGS DFAISGAYTN SDRTNEQNLQ SRGTGKRAEA WATGLKYDAN 240
NIYLATFYSE TRKMTPITGG FANKTQNFEA VAQYQFDFGL RPSLGYVLSK GKDIEGIGDE 300
DLVNYIDVGA TYYFNKNMSA FVDYKINQLD SDNKLNINND DIVAVGMTYQ F 351

<212> Type : PRT
<211> Length : 351
SequenceName : SEQ ID 52
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRVKHAVVLL MLISPLSWAG TMTFQFRNPN FGGNPNNGAF LLNSAQAQNS YKDPSYNDDF 60
GIETPSALDN FTQAIQSQIL GGLLSNINTG KPGRMVTNDY IVDIANRDGQ LQLNVTDRKT 120
GQTSTIQVSG LQNNSTDF 138
<212> Type : PRT
<211> Length : 138
SequenceName : SEQ ID 53
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKRKVLAMLV PALLVAGAAN AAEIYNKDGN KLDLYGKVAG LHYFSDDASS DGDMSYARIG 60
FKGETQIADQ FTGYGQWEFN IGANGPESDK GNTATRLAFA GFGFGQNGTF DYGRNYGVVY 120
DVEAWTDMLP EFGGDTYAGA DNFMNGRANS VATYRNNGFF GQVDGLNFAL QYQGNNEKSG 180
LFDQEGSGNG NGRKLAKENG DGSVCPLPMT LTLV 214
<212> Type : PRT
<211> Length : 214
SequenceName : SEQ ID 54
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MNTVTLEGGT FNNNGTLNDV VKIEKNSNAV INNTGSLSTL QLHDGTVNNS GIASARVNAQ 60
GDAVFNNLAG GEARKGAILY NSAVVNNAGT WKMGYQDENN NAGTLDIDDK STFNNSGKLI 120
LDNSKNAIRF QGSNANATLY NTGEMTLDAA LGAGAILYDD GASEFINKGV VDAKVTVAVS 180
TAGATESDAF LWNQDGGVIN FDKDNASAVK FTHNNYVALN DGVMNISGNN AVAMEGDKNA 240
QLVNNGVINL GTEGTTDTGL TGMQLDANAT ADAVIENNGT INIFANDSFA FSVLGTEGHI 300
VNNGTVVIAD GVTGSGLIKQ GDSVNVEGVN GNSGNNTEVH YTDYTLPDMP NTYTTSPFSE 360
TTDSGSSDGS SNNLNGYIVG TNVDGSAGKL KVNNASMNGV GINTGFAAGT ADTTVSFDNV 420
VEGINLTDAD AITSTSVVWT AKGSTDASGN VDVIMSKNAY TDVATDASVN DVAKALDAGY 480
TNNELYTSLN VGTTAELNSA LKQVSGSQAT TVFREARVLS NRFSMLADAA PKVGNGLAFN 540
VVAKGDPRAE LGNNTEYDML ALRKTVDLSE SQSMSLEYGI ARLDGDGAQK AGDNGVTGGY 600
SQFFGLKHQM SFDNGMRWNN ALRYDVHNLD SSRSVAYGDV SKTADTDVKQ QYLELRSEGA 660
KTFEPREGLK ITPYAGVKLR HSLEGGYQER NAGDFNLSMN SGSETAVDSI VGLKLDYAGK 720
GGWSANATLE GGPNLSYSKS QRTASLAGAG SQHFNVDDGQ KGGGINSLAS VGVKYSSKES 780
SLNLDAYHWK EDGISDKGVM LNFKKTF 807
<212> Type : PRT

<211> Length : 807
SequenceName : SEQ ID 55
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MLNGISNAAS TLGRQLVGIA SRVSSAGGTG FSVAPQAVRL TPVKVHSPFS PGSSNVNART 60
IFNVSSQVTS FTPSRPAPPP PTSGQASGAS RPLPPIAQAL KEHLAAYEKS KGPEALGFKP 120
ARQAPPPPTS GQASGASRPL PPIAQALKEH LAAYEKSKGP EALGFKPARQ APPPPTSGQA 180
SGASRPLPPI AQALKEHLAA YEKSKGPEAL GFKPARQAPP PPTGPSGLPP LAQALKDHLA 240
AYEQSKKG 248
<212> Type : PRT
<211> Length : 248
SequenceName : SEQ ID 56
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MNKKIHSLAL LVNLGIYGVA QAQEPTDTPV SHDDTIVVTA AEQNLQAPGV STITADEIRK 60
NPVARDVSEI IRTMPGVNLT GNSTSGQRGN NRQIDIRGMG PENTLILIDG KPVSSRNSVR 120
QGWRGERDTR GDTSWVPPEM IERIEVLRGP AAARYGNGAA GGVVNIITKK GSGEWHGSWD 180
AYFNAPEHKE EGATKRTNFS LTGPLGDEFS FRLYGNLDKT QADAWDINQG HQSARAGTYA 240
TTLPAGREGV INKDINGVVR WDFAPLQSLE LEAGYSRQGN LYAGDTQNTN SDAYTRSKYG 300
DETNRLYRQN YSLTWNGGWD NGVTTSNWVQ YEHTRNSRIP EGLAGGTEGK FNEKATQDFV 360
DNDLDDVMLH SEVNLPIDFL VNQTLTLGTE WNQQRMKDLS SNTQALTGTN TGGAIDGVSA 420
TDRSPYSKAE IFSLFAENNM ELTDSTIVTP GLRFDHHSIV GNNWSPALNI SQGLGDDFTL 480
KMGIARAYKA PSLYQTNPNY ILYSKGQGCY ASAGGCYLQG NDDLKAETSI NKEIGLEFKR 540
DGWLAGITWF RNDYRNKIEA GYVAVGQNAV GTDLYQWDNV PKAVVEGLEG SLNVPVSETV 600
MWTNNITYML KSENKTTGDR LSIIPEYTLN STLSWQARED LSMQTTFTWY GKQQPKKYNY 660
KGQPAVGPET KEISPYSIVG LSATWDVTKN VSLTGGVDNL FDKRLWRAGN AQTTGDLAGA 720
NYIAGAGAYT YNEPGRTWYM SVNTHF 746
<212> Type : PRT
<211> Length : 746
SequenceName : SEQ ID 57
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MGGRFSLRYK KLSYRFVFLT LAGCSSVGNQ SLKNETQESV KTKIVKGKTT KQDVLASFGE 60
PDSRSLIDGE EQWSYTMYNS QSKATSFIPV VGLLAGGADS QTKSLTVSFK GEKVSTYIFN 120
AGTSNVKTGI F 131
<212> Type : PRT
<211> Length : 131
SequenceName : SEQ ID 58
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKKIACLSAL AAVLAFTAGT SVAATSTVTG GYAQSDAQGQ MNKMGGFNLK YRYEEDNSPL 60
GVIGSFTYTE KSRTASSGDY NKNQYYGITA GPAYRINDWA SIYGVVGVGY GKFQTTEYPT 120
YKHDTSDYGF SYGAGLQFNP MENVALDFSY EQSRIRSVDV GTWIAGVGYR F 171

<212> Type : PRT
<211> Length : 171
SequenceName : SEQ ID 59
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKSIATLVVC AISGIACVNL SAHAAEGEHT ISLGYAHFQF PGLKDFVKDA TAHNRETFSH 60
FVNRNYFSSL GEYTDGRVSG YEGKDKNPQG INIRYRYEIT DDFGVITSFT WTRSLTNSQT 120
FIDVQSADHT RKIKNPAASA RTDIRANYWS LLAGPSWRVN QYMSLYAMAG MGVAKVSADL 180
KIKDNINSSG GFSESNSTKK TSLAWAAGAQ FNLNESVTLD VAYEGSGSGD WRTSGVTAGI 240
GLKF 244
<212> Type : PRT
<211> Length : 244
SequenceName : SEQ ID 60
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRKLYAAILS AAICLTVSGA PAWASEQQAT LSAGYLHVST NAPGSDNLNG INVKYRYEFT 60
DTLGLVTSFS YAGDRNRQIT RYSDTRWHED SVRNRWFSVM AGPSVRVNEW FSAYAMAGVA 120
YSRVSTFSGD YLRVTDNKGK THDVLTGSDD GRHSNTSLAW GAGVQFNPTE SVAIDIAYEG 180
SGSGDWRTDG FIVGVGYKF 199
<212> Type : PRT
<211> Length : 199
SequenceName : SEQ ID 61
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRKLYAAILS AAICLAVSGA PAWASEQQAT LSAGYLHART SAPGSDNLNG INVKYRYEFT 60
DTLGLVTSFS YAGDKNRQLT RYSDTRWHED SVRNRWFSVM AGPSVRVNEW FSAYAMAGVA 120
YSRVSTFSGD YLRVTDNKGK THDVLTGSDD GRHSNTSLAW GAGVQFNPTE SVAIDIAYEG 180
SGSGDWRTDG FIVGVGYKF 199
<212> Type : PRT
<211> Length : 199
SequenceName : SEQ ID 62
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRKLYAAILS AAICLAVSGA PAWASEQQAT LSAGYLHART SAPGSDNLNG INVKYRYEFT 60
DTLGLVTSFS YAGDKNRQLT RYSDTRWHED SVRNRWFSVM AGPSVRVNEW FSAYAMAGVA 120
YSRVSTFSGD YLRVTDNKGK THDVLTGSDD GRHSNTSLAW GAGVQFNPTE SVAIDIAYEG 180
SGSGDWRTDG FIVGVGYKF 199
<212> Type : PRT
<211> Length : 199
SequenceName : SEQ ID 63
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRKLYAAILS AAICLAVSGA PAWASEQQAT LSAGYLHART SAPGSDNLNG INVKYRYEFT 60
DTLGLVTSFS YAGDKNRQLT RYSDTRWHED SVRNRWFSVM AGPSVRVNEW FSAYAMAGVA 120
YSRVSTFSGD YLRVTDNKGK THDVLTGSDD GRHSNTSLAW GAGVQFNPTE SVAIDIAYEG 180
SGSGDWRTDG FIVGVGYKF 199
<212> Type : PRT
<211> Length : 199
SequenceName : SEQ ID 64
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7

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<400> PreSequenceString :
MVMSQKTLFT KSALAVAVAL ISTQAWSAGF QLNEFSSSGL GRAYSGEGAI ADDAGNVSRN    60
PALITMFDRP TFSAGAVYID PDVNISGTSP SGRSLKADNI APTAWVPNMH FVAPINDQFG   120
WGASITSNYG LATEFNDTYA GGSVGGTTDL ETMNLNLSGA YRLNNAWSFG LGFNAVYARA   180
KIERFAGDLG QLVAGQIMQS PAGKTPQGQA LAATANGIDS NTKIAHLNGN QWGFGWNAGI   240
LYELDKNNRY ALTYRSEVKI DFKGNYSSDL NRVFNNYGLP IPTATGGATQ SGYLTLNLPE   300
MWEVSGYNRV DPQWAIHYSL AYTSWSQFQQ LKATSTSGDT LFQKHEGFKD AYRIALGTTY   360
YYDDNWTFRT GIAFDDSPVP AQNRSISIPD QDRFWLSAGT TYAFNKDASV DVGVSYMHGQ   420
SVKINEGPYQ FESEGKAWLF GTNFNYAF                                      448
<212> Type : PRT
<211> Length : 448
      SequenceName : SEQ ID 65
      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MAFSQAVSGL NAAATNLDVI GNNIANSATY GFKSGTASFA DMFAGSKVGL GVKVAGITQD    60
FTDGTTTNTG RGLDVAISQN GFFRLVDSNG SVFYSRNGQF KLDENRNLVN MQGLQLTGYP   120
ATGTPPTIQQ GANPTNISIP NTLMAAKTTT TASMQINLNS SDPLPSVNAF DASNADSYNK   180
KGSVTVFDSQ GNAHDMSVYF VKTGDNNWQV YTQDSSDPTG TAEPAMKLVF NANGVLTSNP   240
TENITTGAIN GAEPATFSLS FLNSMQQNTG ANNIVATTQN GYKPGDLVSY QINDDGTVVG   300
NYSNEQTQLL GQIVLANFAN NEGLASEGDN VWSATQSSGV ALLGTAGTGN FGTLTNGALE   360
ASNVDLSKEL VNMIVAQRNY QSNAQTIKTQ DQILNTLVNL R                       401
<212> Type : PRT
<211> Length : 401
      SequenceName : SEQ ID 66
      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSKSTFLHIL ISSIILVALI QSSAWANCTN TQIGQTEDGR TALIEFGKIN MTDTYFAPAG    60
SLLATTVVPP TNYTSGGATG SSVLWECDAT DLPNIYFLVA TNGDDRVGGF YDAGGPDGLS   120
DVYATWFAFV GLKQTMAGVT LGRYWKKVPI TSYATQGTKI QIRLQDIPPL HAELYRISTL   180
PDTSATTSWC GNNNTDSSGV GFAKPSGTIY NCVQPNAYIQ LSGTSGILFG HDEPGEDSSV   240
HWDFWGADNG FGYGMRSANR LYNNATCVAR SATPLVLLPT IAEAQLNAGM ESTGNFNVRV   300
ECSNSVQSGI SDTQTALGIQ VSEGAYTAAQ KLGIINSNGG VSALVSDNYD AAEMAKGVGI   360
YISNSAHPDT AMTLVGQPGI AKLTPGGNAA GWYPVFEGAT LEGATHPGYS SYSYSFIARL   420
KKLPNQTVSA GKVRATAYIL VKMQ                                          444
<212> Type : PRT
<211> Length : 444
      SequenceName : SEQ ID 67
      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MENNRNFPAR QFHSLTFFAG LCIGITPVAQ ALAAEGQTNA DDTLVVEAST PSLYAPQQSA    60
DPKFSRPVAD TTRTMTVISE QVIKDQGATN LTDALKNVPG VGAFFAGENG NSTTGDAIYM   120
RGADTSNSIY IDGIRDIGSV SRDTFNTEQV EVIKGPSGTD YGRSAPTGSI NMISKQPRND   180
SGIDASASIG SAWFRRGTLD VNQVIGDTTA VRLNVMGEKT HDAGRDKVKN ERYGVAPSIA   240
FGLGTANRLY LNYLHVTQHN TPDGGIPTIG LPGYSAPSAG TATLNHSGKV DTHNFYGTDS   300
DYDDSTTDTA TMRFEHDIND NTTIRNTTRW SRVKQDYLMT AIMGGASNIT QPTSDVNSWT   360
WSRTANTKDV SNKILTNQTN LTSTFYTASI GHDVSTGVEF TRETQTNYGV NPVTLPAVNI   420
YHPDSSIHPG GLTRNGANAN GQTDTFAIYA FDTLQITRDF ELNGGIRLDN YHTEYDSATA   480
CGGSGRGAIT CPAGVAKGSP VTTVDTAKSG NLVNWKAGAL YHLTENGNVY INYAVSQQPP   540
GGNNFALAQS GSGNSANRTD FKPQKANTSE IGTKWQVLDK RLLLTAALFR TDIENEVEQN   600
DDGTYSQYGK KRVEGYEISV AGNITPAWQV IGGYTQQKAT IKNGKDVAQD GSSSLPYTPE   660
HAFTLWSQYQ ATDDISVGAG ARYIGSMHKG SDGAVGTPAF TEGYWVADAK LGYRVNRNLD   720
FQLNVYNLFD TDYVASINKS GYRYHPGEPR TFLLTANMHF                         760
<212> Type : PRT
<211> Length : 760
      SequenceName : SEQ ID 68
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SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MQMKKLLPIL IGLSLSGFSS LSQAENLMQV YQQARLSNPE LRKSAADRDA AFEKINEARS 60
PLLPQLGLGA DYTYSNGYRD ANGINSNATS ASLQLTQSIF DMSKWRALTL QEKAAGIQDV 120
TYQTDQQTLI LNTATAYFNV LNAIDVLSYT QAQKEAIYRQ LDQTTQRFNV GLVAITDVQN 180
ARAQYDTVLA NEVTARNNLD NAVEQLRQIT GNYYPELAAL NVENFKTDKP QPVNALLKEA 240
EKRNLSLLQA RLSQDLAREQ IRQAQDGHLP TLDLTASSGI SDTSYSGSKT RGAAGTQYDD 300
SNMGQNKVGL SFSLPIYQGG MVNSQVKQAQ YNFVGASEQL ESAHRSVVQT VRSSFNNINA 360
SISSINAYKQ AVVSAQSSLD AMEAGYSVGT RTIVDVLDAT TTLYNAKQEL ANARYNYLIN 420
QLNIKSALGT LNEQDLLALN NALSKPVSTN PENVAPQTPE QNAIADGYAP DSPAPVVQQT 480
SARTTTSNGH NPFRN 495
<212> Type : PRT
<211> Length : 495
SequenceName : SEQ ID 69
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MTKLKLLALG VLIATSAGVA HAEGKFSLGA GVGVVEHPYK DYDTDVYPVP VINYEGDNFW 60
FRGLGGGYYL WNDATDKLSI TAYWSPLYFK AKDSGDHQMR HLDDRKSTMM AGLSYAHFTQ 120
YGYLRTTLAG DTLDNSNGIV WDMAWLYRYT NGGLTVTPGI GVQWNSENQN EYYYGVSRKE 180
SARSGLRGYN SNDSWSPYLE LSASYNFLGD WSVYGTARYT RLSDEVTDSP IVDKSWTGLI 240
STGITYKF 248
<212> Type : PRT
<211> Length : 248
SequenceName : SEQ ID 70
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKKTLLAAGA VLALSSSFTV NAAENDKPQY LSDWWHQSVN VVGSYHTRFG PQIRNDTYLE 60
YEAFAKKDWF DFYGYADAPV FFGGNSDAKG IWNHGSPLFM EIEPRFSIDK LTNTDLSFGP 120
FKEWYFANNY IYDMGRNKDG RQSTWYMGLG TDIDTGLPMS LSMNVYAKYQ WQNYGAANEN 180
EWDGYRFKIK YFVPITDLWG GQLSYIGFTN FDWGSDLGDD SGNAINGIKT RTNNSIASSH 240
ILALNYDHWH YSVVARYWHD GGQWNDDAEL NFGNGNFNVR STGWGGYLVV GYNF 294

<212> Type : PRT
<211> Length : 294
SequenceName : SEQ ID 71
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MLSTQFNRDN QYQAITKPSL LAGCIALALL PSAAFAAPAT EETVIVEGSA TAPDDGENDY 60
SVTSTSAGTK MQMTQRDIPQ SVTIVSQQRM EDQQLQTLGE VMENTLGISK SQADSDRALY 120
YSRGFQIDNY MVDGIPTYFE SRWNLGDALS DMALFERVEV VRGATGLMTG TGNPSAAINM 180
VRKHATSREF KGDVSAEYGS WNKERYVADL QSPLTEDGKI RARIVGGYQN NDSWLDRYNS 240
EKTFFSGIVD ADLGDLTTLS AGYEYQRIDV NSPTWGGLPR WNTDGSSNSY DRARSTAPDW 300
AYNDKEINKV FMTLKQRFAD TWQATLNATH SEVEFDSKMM YVDAYVNKAD GMLVGPYSNY 360
GPGFDYVGGT GWNSGKRKVD ALDLFADGSY ELFGRQHNLM FGGSYSKQNN RYFSSWANIF 420
PDEIGSFYNF NGNFPQTDWS PQSLAQDDTT HMKSLYAATR VTLADPLHLI LGARYTNWRV 480
DTLTYSMEKN HTTPYAGLVF DINDNWSTYA SYTSIFQPQN DRDSSGKYLA PITGNNYELG 540
LKSDWMNSRL TTTLAIFRIE QDNVAQSTGT PIPGSNGETA YKAVDGTVSK GVEFELNGAI 600
TDNWQLTFGA TRYIAEDNEG NAVNPNLPRT TVKMFTSYRL PVMPELTVGG GVNWQNRVYT 660
DTVTPYGTFR AEQGSYALVD LFTRYQVTKN FSLQGNVNNL FDKTYDTNVE GSIVYGAPRN 720
FSITGTYQF 729
<212> Type : PRT

<211> Length : 729
SequenceName : SEQ ID 72
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MARFQFKNRK NNGLIFFISF MVMGEAAIAA PLPQWANAPA VTPVAQLSLQ ESILRAFARN 60
PGVTQQAAQI GIGEAQIDEA KSAWYPHVGL TGNAGPSRQT DSSGRLDNNV SYGITLTQLV 120
YDFGKTNNDI NLQTAARDSY RFKLMATLTD VAEKTATAYM EVSRYQALCD AAQRNIHSLE 180
NVYNMAALRA NAGLNSSSDE LQAQTRIAGM RSTLEQYQAQ MASAKAQLAV LTGVQPEAIA 240
APPAELAEQP VSLKNIDYQS IPLVLAAENL RQSAQYGVEK TKAQYWPTLS IQGGKTRYQT 300
SDRSYWDDQL QLNVNAPLYQ GGAVSAQVQQ AEGQQKISAS QVEQAKLDVL QRASVAYANW 360
TGARGREEAG LAQSESAHKT RDVYQNEYKL GKRSLNDLLT VEQDVFQAQS AEINANYDGW 420
VAAVNYAAAV NNLIPLAGIK QGLYNDLPDL K 451
<212> Type : PRT
<211> Length : 451
SequenceName : SEQ ID 73
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MAKFTPSFSG IKGRALFSLL FAAPMIHATD TATTKDGETI TVTADANTAT EATDGYQPLS 60
TSTATLTDMP MLDIPQVVNT VSDQVLENQN ATTLDEALYN VSNVVQTNTL GGTQDAFVRR 120
GFGANRDGSI MTNGLRTVLP RSFNAATERV EVLKGPASTL YGILDPGGLI NVVTKRPEKT 180
FHGSVSATSS SFGGGTGQLD ITGPIEGTQL AYRLTGEVQD EDYWRNFGKE RSTFIAPSLT 240
WFGDNATVTM LYSHRDYKTP FDRGTIFDLT TKQPVNVDRK IRFDEPFNIT DGQSDLAQLN 300
AEYHLNSQWT ARFDYSYSQD KYSDNQARVT AYDATTGTLT RRVDATQGST QRMHSTRADL 360
QGNVDIAGFY NEILGGVSYE YYDLLRTDMI RCKNAKDFNI YNPVYGNTSK CTTVSASDSD 420
QTIKQESYSA YAQDALYLTD NWIAVAGIRY QYYTQYAGKG RPFNVNTDSR DEQWTPKLGL 480
VYKLTPSVSL FANYSQTFMP QSSIASYIGD LPPESSNAYE VGAKFELFDG ITADIALFDI 540
HKRNVLYTES IGDETIAKTA GRVRSRGVEV DLAGALTENI NIIASYGYTD AKVLEDPDYA 600
GKPLPNVPRH TGSLFLTYDI HNMPGNNTLT FGGGGHCVSR RSATNGADYY LPGYFVADAF 660
AAYKMKLQYP VTLQLNVKNL FDKTYYTSSI ATNNLGNQIG DPREVQFTVK MEF 713

<212> Type : PRT
<211> Length : 713
SequenceName : SEQ ID 74
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRTLQGWLLP VFMLPMAVYA QEATVKEVHD APAVRGSIIA NMLQEHDNPF TLYPYDTNYL 60
IYTQTSDLNK EAIASYDWAE NARKDEVKFQ LSLAFPLWRG ILGPNSVLGA SYTQKSWWQL 120
SNSEESSPFR ETNYEPQLFL GFATDYRFAG WTLRDVEMGY NHDSNGRSDP TSRSWNRLYT 180
RLMAENGNWL VEVKPWYVVG NTDDNPDITK YMGYYQLKIG YHLGDAVLSA KGQYNWNTGY 240
GGAELGLSYP ITKHVRLYTQ VYSGYGESLI DYNFNQTRVG VGVMLNDLF 289
<212> Type : PRT
<211> Length : 289
SequenceName : SEQ ID 75
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MAVQKNVIKG ILAGTFALML SGCVTVPDAI KGSSPTPQQD LVRVMSAPQL YVGQEARFGG 60
KVVAVQNQQG KTRLEIATVP LDSGARPTLG EPSRGRIYAD VNGFLDPVDF RGQLVTVVGP 120
ITGAVDGKIG NTPYKFMVMQ ATGYKRWHLT QQVIMPPQPI DPWFYGGRGW PYGHGGWGWY 180
NPGPARVQTV VTE 193
<212> Type : PRT
<211> Length : 193

SequenceName : SEQ ID 76
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MRKQWLGICI AAGMLAACTS DDGQQQTVSV PQPAVCNGPI VEISGADPRF EPLNATANQD 60
YQRDGKSYKI VQDPSRFIQA GLAAIYDAEP GSNLTASGEA FDPTQLTAAH PTLPIPSYAR 120
ITNLANGRMI VVRINDRGPY GNDRVISLSR AAADRLNTSN NTKVRIDPII VAQDGSLSGP 180
GMACTTVAKQ TYALPAPPDL SGGAGTSSVS GPQGDILPVS NSTLKSEDPT GAPVTSSGFL 240
GAPTTLAPGV LEGSEPTPAP QPVVTAPSTT PATSPAMVTP QAASQSASGN FMVQVGAVSD 300
QARAQQYQQQ LGQKFGVPGR VTQNGAVWRI QLGPFANKAE ASTLQQRLQT EAQLQSFITT 360
AQ 362
<212> Type : PRT
<211> Length : 362
SequenceName : SEQ ID 77
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MIKRVLVVSM VGLSLVGCVN NDTLSGDVYT ASEAKQVQNV SYGTIVNVRP VQIQGGDDSN 60
VIGAIGGAVL GGFLGNTVGG GTGRSLATAA GAVAGGVAGQ GVQSAMNKTQ GVELEIRKDD 120
GNTIMVVQKQ GNTRFSPGQR VVLASNGSQV TVSPR 155
<212> Type : PRT
<211> Length : 155
SequenceName : SEQ ID 78
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MSKATEQNDK LKRAIIISAV LHVILFAALI WSSFDENIEA SAGGGGGSSI DAVMVDSGAV 60
VEQYKRMQSQ ESSAKRSDEQ RKMKEQQAAE ELREKQAAEQ ERLKQLEKER LAAQEQKKQA 120
EEAAKQAELK QKQAEEAAAK AAADAKAKAE ADDKAAEEAA KKAAADAKKK AEAEAAKAAA 180
EAQKKAEAAA AALKKKAEAA EAAAAEARKK AAAEKAAADK KAAEKAAAEK AAADKKAAAE 240
KAAADKKAAA AKAAAEKAAA AKAAAEADDI FGELSSGKNA PKTGGGAKGN NASPAGSGNT 300
KNNGASGADI NNYAGQIKSA IESKFYDASS YAGKTCTLRI KLAPDGMLLD IKPEGGDPAL 360
CQAALAAAKL AKIPKPPSQA VYEVFKNAPL DFKP 394
<212> Type : PRT
<211> Length : 394
SequenceName : SEQ ID 79
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MMKFKKCLLP VAMLASFTLA GCQSNADDHA ADVYQTDQLN TKQETKTVNI ISILPAKVAV 60
DNSQNKRNAQ AFGALIGAVA GGVIGHNVGS GSNSGTTAGA VGGGAVGAAA GSMVNDKTLV 120
EGVSLTYKEG TKVYTSTQVG KECQFTTGLA VVITTTYNET RIQPNTKCPE KS 172

<212> Type : PRT
<211> Length : 172
SequenceName : SEQ ID 80
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MLLSIITVAF RNLEGIVKTH ASLAHLAQAE DISFEWIVVD GGSNDGTREY LENLNGIYNL 60
RFVSEPDNGI YDAMNKGIAM AQGKFALFLN SGDIFHQDAA YFVRKLKMQK DNVMITGDAL 120
LDFGDGHKIK RSAKPGWYIY HSLPASHQAI FFPVSGLKKW RYDLEYKVSS DYALAAKMYK 180

AGYAFKKLNG LVSEFSMGGV STTNNMELCA DAKKVQRQIL HVPGFWAELS WHLRQRTTSK 240
TKALYNKS 248
<212> Type : PRT
<211> Length : 248
SequenceName : SEQ ID 81
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MKLTTLQTLK KGFTLIELMI VIAIIAILAT IAIPSYQNYT KKAAVSELLQ ASAPYKADVE 60
LCVYSTNETT SCTGGKNGIA ADIKTAKGYV ASVITQSGGI TVKGNGTLAN MEYILQAKGN 120
AAAGVTWTTT CKGTDASLFP ANFCGSVTK 149
<212> Type : PRT
<211> Length : 149
SequenceName : SEQ ID 82
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MLNKKFKLNF IALTVAYALT PYTEAALVRD DVDYQIFRDF AENKGRFSVG ATNVEVRDKN 60
NHSLGNVLPN GIPMIDFSVV DVDKRIATLI NPQYVVGVKH VSNGVSELHF GNLNGNMNNG 120
NAKSHRDVSS EENRYFSVEK NEYPTKLNGK AVTTEDQTQK RREDYYMPRL DKFVTEVAPI 180
EASTASSDAG TYNDQNKYPA FVRLGSGSQF IYKKGDNYSL ILNNHEVGGN NLKLVGDAYT 240
YGIAGTPYKV NHENNGLIGF GNSKEEHSDP KGILSQDPLT NYAVLGDSGS PLFVYDREKG 300
KWLFLGSYDF WAGYNKKSWQ EWNIYKPEFA KTVLDKDTAG SLTGSNTQYN WNPTGKTSVI 360
SNGSESLNVD LFDSSQDTDS KKNNHGKSVT LRGSGTLTLN NNIDQGAGGL FFEGDYEVKG 420
TSDSTTWKGA GVSVADGKTV TWKVHNPKSD RLAKIGKGTL IVEGKGENKG SLKVGDGTVI 480
LKQQADANNK VKAFSQVGIV SGRSTVVLND DKQVDPNSIY FGFRGGRLDA NGNNLTFEHI 540
RNIDDGARLV NHNTSKTSTV TITGESLITD PNTITPYNID APDEDNPYAF RRIKDGGQLY 600
LNLENYTYYA LRKGASTRSE LPKNSGESNE NWLYMGKTSD EAKRNVMNHI NNERMNGFNG 660
YFGEEEGKNN GNLNVTFKGK SEQNRFLLTG GTNLNGDLKV EKGTLFLSGR PTPHARDIAG 720
ISSTKKDQHF AENNEVVVED DWINRNFKAT NINVTNNATL YSGRNVANIT SNITASDNAK 780
VHIGYKAGDT VCVRSDYTGY VTCTTDKLSD KALNSFNATN VSGNVNLSGN ANFVLGKANL 840
FGTISGTGNS QVRLTENSHW HLTGDSNVNQ LNLDKGHIHL NAQNDANKVT TYNTLTVNSL 900
SGNGSFYYLT DLSNKQGDKV VVTKSATGNF TLQVADKTGE PTKNELTLFD ASNATRNNLN 960
VSLVGNTVDL GAWKYKLRNV NGRYDLYNPE VEKRNQTVDT TNITTPNNIQ ADVPSVPSNN 1020
EEIARVETPV PPPAPATPSE TTETVAENSK QESKTVEKNE QDATETTAQN GEVAEEAKPS 1080
VKANTQTNEV AQSGSETEET QTTEIKETAK VEKEEKAKVE KDEIQEAPQM ASETSPKQAK 1140
PAPKEVSTDT KVEETQVQAQ PQTQSTTVAA AEATSPNSKP AEETQPSEKT NAEPVTPVVS 1200
KNQTENTTDQ PTEREKTAKV ETEKTQEPPQ VASQASPKQE QSETVQPQAV LESENVPTVN 1260
NAEEVQAQLQ TQTSATVSTK QPAPENSINT GSATAITETA EKSDKPQTET AASTEDASQH 1320
KANTVADNSV ANNSESSDPK SRRRRSISQP QETSAEETTA ASTDETTIAD NSKRSKPNRR 1380
SRRSVRSEPT VTNGSDRSTV ALRDLTSTNT NAVISDAMAK AQFVALNVGK AVSQHISQLE 1440
MNNEGQYNVW VSNTSMNENY SSSQYRRFSS KSTQTQLGWD QTISNNVQLG GVFTYVRNSN 1500
NFDKASSKNT LAQVNFYSKY YADNHWYLGI DLGYGKFQSN LKTNHNAKFA RHTAQFGLTA 1560
GKAFNLGNFG ITPIVGVRYS YLSNANFALA KDRIKVNPIS VKTAFAQVDL SYTYHLGEFS 1620
VTPILSARYD TNQGSGKINV NQYDFAYNVE NQQQYNAGLK LKYHNVKLSL IGGLTKAKQA 1680
EKQKTAELKL SFSF 1694
<212> Type : PRT
<211> Length : 1694
SequenceName : SEQ ID 83
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MALVNKIKTL SSVGILAATL FLAGCQAQSN ILAFTPPAPS ASMNVNRTAV VSVTTKDSRA 60
IQEIASYTKH GELIKLNASP SVTQLFQQVM QQNLISKGFR VGQLNGSNAW VTVDVREFGT 120
QVEQGNLRYK LNTKIQATVY VQGAKGSYNK SFNVTHSQEG VFNAGNDEIH KVLSQTFNDI 180
VNNIYQDQEV AAAINQYSN 199
<212> Type : PRT
<211> Length : 199

SequenceName : SEQ ID 84
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MLCWIGYKNG ILPQQNSTLY PWLNPSKCGV IFDGFQLVGD DFNSDQTAEN TSPAWQVLYT 60
THLQSCSPIH SGENFAPIPL YKQLKNQPHL SQDLIKWQEN WQACDQLQMN GAVLEQQSLA 120
EISDHQSTLS KHGRYLAQEI EKETGIPTYY YLYRVGGQSL ESEKSRCCPS CGANWALKDA 180
IFDTFHFKCD TCRLVSNLSW NFL 203
<212> Type : PRT
<211> Length : 203
SequenceName : SEQ ID 85
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MGAFAFASVT NANIYAEGDI GLSQTKANGS NNTRVGPRVS VGYKVGNTRV AGDYTHHGKV 60
DGTKIQGLGA SVLYDFDTNS KVQPYVGARV ATNQFKYTNR AEQKFKSSSD IKLGYGVVAG 120
AKYKLDGNWY ANGGVEYNRL GNFDSTKVNN YGAKVGVGYG F 161
<212> Type : PRT
<211> Length : 161
SequenceName : SEQ ID 86
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
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VRSLFVSGRF DDVKAHQEGD VLVVSVVAKS IISDVKIKGN SIIPTEALKQ NLDANGFKVG 120
DVLIREKLNE FAKSVKEHYA SVGRYNATVE PIVNTLPNNR AEILIQINED DKAKLASLTF 180
KGNESVSSST LQEQMELQPD SWWKLWGNKF EGAQFEKDLQ SIRDYYLNNG YAKAQITKTD 240
VQLNDEKTKV NVTIDVNEGL QYDLRSARII GNLGGMSAEL EPLLSALHLN DTFRRSDIAD 300
VENAIKAKLG ERGYGSATVN SVPDFDDANK TLAITLVVDA GRRLTVRQLR FEGNTVSADS 360
TLRQEMRQQE GTWYNSQLVE LGKIRLDRTG FFETVENRID PINGSNDEVD VVYKVKERNT 420
GSINFGIGYG TESGISYQAS VKQDNFLGTG AAVSIAGTKN DYGTSVNLGY TEPYFTKDGV 480
SLGGNVFFEN YDNSKSDTSS NYKRTTYGSN VTLGFPVNEN NSYYVGLGHT YNKISNFALE 540
YNRNLYIQSM KFKGNGIKTN DFDFSFGWNY NSLNRGYFPT KGVKASLGGR VTIPGSDNKY 600
YKLSADVQGF YPLDRDHLWV VSAKASAGYA NGFGNKRLPF YQTYTAGGIG SLRGFAYGSI 660
GPNAIYAEHG NGNGTFKKIS SDVIGGNAIT TASAELIVPT PFVSDKSQNT VRTSLFVDAA 720
SVWNTKWKSD KSGLDNNVLK SLPDYGKSSR IRASTGVGFQ WQSPIGPLVF SYAKPIKKYE 780
NDDVEQFQFS IGGSF 795
<212> Type : PRT
<211> Length : 795
SequenceName : SEQ ID 87
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MLKKTSLIFT ALLMTGCVQN ANVTTPQAQK MQVEKVDKAL QKGEADRYLC QDDRVVRVVH 60
ATHKKYKKNL HYVTVTFQGV SEKLTLMISE RGKNYANIRW MWQERDDFST LKTNLGEILA 120
TQCVSQTSER LSGQ 134
<212> Type : PRT
<211> Length : 134
SequenceName : SEQ ID 88
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :

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QPTNQNSNVS EQLEQINVSG STENSDTKTP PKIAETVKTA KTLEREQANN IKDIVKYETG 120
VTVVEAGRFG QSGFAIRGVD ENRVAINIDG LRQAETLSSQ GFKELFEGYG NFNNTRNGAE 180
IETLKEVNIT KGADSIKNGS GSLGGSVIYK TKDARDYLIN KDYYVSYKKG YATENNQSFD 240
TLTLAGRYKK FDVLVVTTSR NGHELENYGY KNYNDKIQGK KREKADPYKI EQDSTLLKLS 300
FNPTENHRFT FAADLYEHRS RGQDLSYTLK YQRSGNETPE VDSRHTNDKT KRRNISFSYE 360
NFSQTPFWDT LKLTYSDQRI KTRARTDEYC DAGVRHCEGT DNPTGLKVTN GKITRRDGSD 420
LQFEEKNNTA KSSDKTYDFK KFIDTDKRVI DDKLVLNNPS DTWYDCSIFN CENNAKIKVF 480
KGNNYYGYDG KWKEVDLEIK ELNGKKFAKI KDNDRKIKSI LPSSPGYLER LWQERDLDTN 540
TQQLNLDLTK DFKIWHIEHN LQYGGSYNTA MKRMVNRAGN DASDVQWWAT PTLGEDSWTG 600
KPHTCATTYE WNANLCPRVD PEFSYLLPIK TTGKSVYLFD NFVITDYLSF DLGYRYDNIH 660
YQPKYKHGIT PKLPDDIVKG LFIPLPNNSN SDPNKVKENV QQNIDYIAKQ NKKYKAHSYS 720
FVSTIDPTSF LRLQLKYSKG FRTPTSDEMY FTFKHPDFTI LPNTDLKPEI AKTKEIAFTL 780
HNDDWGFIST SLFKTNYKNF IDLIFKKQET FKVGGSGRGE TLPFSLYQNI NRDNASLKGI 840
EINSKVFLGK MAKFMDGFNL SYKYTYQKGR MNGNIPMNAI QPRTMVYGLG YDHPNHKFGF 900
DFYTTHVASK NPEDTYNMFY KEENKKDSTI KWRSKSYTIL DLIGYVQPIK NLTIRAGVYN 960
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<212> Type : PRT
<211> Length : 1010
SequenceName : SEQ ID 89
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :

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LGFVSALSAQ SEDYNSSVYW LNSVNENNNN KSYYISPLRT WAGGNRSFTQ NYNNSQLYIG 120
TKNASATPNH SSVWFGEKGY IGFITGVFKA RDIFITGAVG SGNELKTGGG AILVFESSNE 180
LTTNGAYFQN NRAGTQTSWI NLISNNSVNL TNTDFGNQTP NGGFNVMGRK ITYNGGSVNG 240
GNFGFDNVDS NGATTISGVT FNNNGALTYK GGNGIGGSIT FTNSNINHYK LNLNANSVTF 300
NNSTLGSMPN GNANTIGNAY ILNANNITFN NLTFNGGWFV FNRSDAHVNF QGTTTINNPT 360
SPFVNMTGKV TINPNAIFNI QNYTPTIGNA YTLFSMKNGN IAYDDVNNLW NIIRLKNTQA 420
TKDNSKNATS NNNTHTYYVT YNLGGTLYHF RQIFSPDSIV LQSVYYGANN LYYTNSVNIH 480
DNVFNLKNIN DDRADTIFYL NGLNTWNYTQ ARFAQTYGGK NSALVFNATT PWANGAIPKS 540
NSTVRFGGYE GVNWGKTGYI TGTFTADRVY ITGNMMSGNG AQTGGGATLN FVGATEINIA 600
GATFKNLKTT SQNSYMTFMA LGNGSGSGKI NVSQSDFYDW TDGGYDFTGN GVFDSVNFNK 660
AYYKFQGAEN SYNFKNTNFL AGNFKFQGKT TIEKSVLNDA SYAFDGVNNA FNEDKFNGGS 720
FNFNHAEQTN AFNNNSFSGG SFSFNAKQVD FNGNSFNGGV FNFNNTPKAS FTNDTFNVNN 780
QFKINGAQTD FTFSKGVVFN MQGLLSSLSV GTTYQLLNAK SVGYKDNNNA LYQMLRWTSG 840
ENPSGKLVDE NKTAPNSAKI YNVQFTDNGL TYYIKENFNN GITLTRLCTL GYTHCVNIDN 900
DAFNLKNVNN NASNTVFYLN GMTTWKTAGT GVFTQDYSGT NSVLVFNQTT PFLAGANPTS 960
NSVVGFGKTS GAEWGLVGYI QGVFKANQID ITGTIRSGNG AKTGGGATLV FNAQERLNIA 1020
NANLNNDKAG LQNSWMNFIV NNGNLNVTNA NFSNQTPHGG FNLKANNITW DKGSVSGGGN 1080
FGVDNANANG NAVIKNVNFS DNGTLIYKGG ENSAGNSLTL ENNTFNSYNI NAKAQNLIFN 1140
NNSFNSGSYS FNDTKNVTFK GTNTLINSDP FSRLKGSVSI DNNSIFNIER DLTDKTTYTL 1200
LSGDNIKYNN QALADNVFSK NLWDLIHYDG EQGTLLRTDN NTYFVQFTQS NGQKFVFEET 1260
FNPGSITYKY FTIHSSPFHT EADSKDIWNQ VRKQFDFIPG KTPVCVGVCY IAPYKNQDLI 1320
GSSAFAWSLN FGATVVGTLL LGSAQEKANN NGGSIWFGKN NLLYLHGNFN ATNIFLTNNF 1380
NVGNPNAGGG ATINFNADET LSADGLNYTN FQTVAMGLQT SASQHSWANF NSKLSMEIKN 1440
SNFRDFTWGG FRFNSGRITF ENTTFSGWTN INGATESGSS YVNMVANTDL IFTDSILGGG 1500
IRYDLKANNI IFNNTQMVVD VSKNVNQSSL NGNVTFNHSR LSVKPNAAIN IGGDQTQTTL 1560
ENASSLSFYN DSVANFNGTT AFNGVSYLNL NPNAQVSFNQ ANFNNANVTF YGIPLFGKTP 1620
NFGNSVRLIN FKGDAKFNQA TLNLRAKNIH LNFQGASTFE NNSTMNLAES SQASFNALSV 1680
EGETNFNLNG SSLLSFNGNS VFNAPVNFYA NNSQISFTHS ATFNADASFD LGNNSTLNFQ 1740
SVLLNSALNL LGNGGNNLAI NAKGNFSFGS QGILNLSYMN LFGGDKKASV YDVLQAQNID 1800
GLRGNNGYEK IRFYGIQIEK ADYSFNNGVH SWSFTNPLNT TETITETLHN NRLKVQISQN 1860
GASNNAMFNL APSLYDYQQN PYDESENSYN HTSDKAGTYY LSSSIKGFGK NNEIPGTYNA 1920
QNQPLQALHI YNQAISKQDL NMIASLGKEF LPKVAKLIAS GALDNLNLNS PDSFETIFSI 1980
LKEYGITLNQ ANWKSLLKII NNFSNTANYH FSQGSLVVGA IKEGQTNTNS VVWFGGDGYK 2040
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VSFESATNLV LNQANIDAQG TDKIFSYLGK EGIDKLFGEK GLGNVLSNIV YEESLNDNAI 2160
PKDLANMIPK DLGSKTLSSL LSPTEVNNLL GVSAFKNAIM EILNSKTVGD VFGENGLLNA 2220
LDPVKRKEID QMLLEQIQAH SSGFEKFIVK TLGIENVENF INNWYGKQSL SSFANNFVPG 2280
GLNQALDKIG SSSDAKDLQS FLDKTTFGDI LNQMINQAPL INKLISWLGP QDLSVLVNIA 2340
LNSITNPSKE LLGAISGMGQ KVLNDLLGEG VVNKIMSNQV LGQMINKIIA DKGFGGVYHQ 2400
GLGSILPKSL QDELKKLGMG SLLKPKGLHN LWQKGNFNFV AKNHVFVNNS LFSNATGGEL 2460

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NFVAGKSIIF NGKNTINFTQ YQGRLSFVSK DFSNISLDTL NATNGLTLNA SKNDISVQKG   2520
QICVNVLDCM TAKGKTTQTN SSSSATAPTN ETLEVSANNF AFLGTIKANG LVDFSKVLQN   2580
TTIGTLDLGP NATFKANNLI VNNAFNNNSN YRANISGNFN VAKGATFSTN ENGLNVGGNF   2640
NSEGPLIFNL NNPTHQTIIN VTGTSTIMSY NNQALINFNT QLKQGAYTLI NANRMVYGYD   2700
NQTILGGSLS DYLKLYTLID FNGKRMQLNG DSLSYDNQPV SIKDGGLVVS FKDNQGQMVY   2760
SSILYDKIQV TVSDKPMSIQ APSLEYYVKR IQGSAGLNAI KSAGNNSIMW LSELFAAKGG   2820
NPLFAPYYLQ DNPTEHIVTL MKDITSALGM LSNSNLKNNS TDVLQLNTYT QQMSRLAKLS   2880
NFASFDSTDF SERLSSLKNQ RFADAVPNAM DVILKYSQRD KLKNNLWATG VGGVSFVENG   2940
TGTLYGVNVG YDRFVRGVIV GGYAAYGYSG FYERITSSKS DNVDVGLYAR AFIKKSELTF   3000
SVNETWGANK TQISSNDALL SMINQSYKYS TWTTNAKVNY GYDFMFKNKS IILKPQIGLR   3060
YYYIGMSGLE GVMNNVLYNQ FKANADPSKK SVLTIDFALE NRHYFNTNSY FYAIGGVGRD   3120
LLVNSMGDKL VRFIGNNTLS YRKGDLYNTF ANITTGGEVR LFKSFYANAG VGARFGLDYK   3180
MIDIIGNIGM RLAF                                                     3194
<212> Type : PRT
<211> Length : 3194
      SequenceName : SEQ ID 90
      SequenceDescription :

Sequence
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<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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VHRPWYAIWS CDKWEEKTQQ FTGNQLITKT WAGGNAANYY HSQNNQDITA NLKNDNGTYF    120
LSGLYNYTGG EYNGGNLDIE LGSNATFNLG ASSGNSFTSW YPNGHTDVTF SAGTINVNNS    180
VEVGNRVGSG AGTHTGTATL NLNANKVTIN SNISAYKTSQ VNVGNANSVI TINSVSLNGD    240
TCSSLARVGV GANCSTSGPS YSFKGTTNAT NTTFSNSSGS FTFEENATFS GAKLNGGAFT    300
FNKKFNATNN TAFNSGSFTF KGTSSFNGAN FSNASYTFNN QATFQNSSFN GGTFTFNDQT    360
NQSTQHPQIQ NSSFSGSATT LKGFATFEQA FNNSNHQLTI QNASFNNATF NNTGKITIEK    420
DASFNNTSFN TPVDTNNMTI SGGVTLSGKN DLKNGATLDF GSSKITLTQG TTFNLTSLGS    480
EKSVTILNSR GGITYNHLLN HAINSLTNAL KTNESSSKPQ SFAQGLWDMI TYNGVTGQLL    540
NENAATSKPT DSSPSKSSTN STQVYQVGYK IGDTIYKLQE TFSHNSIIIQ ALESGTYTPP    600
PVINGSKFDL SASNYINADM PWYNHKYYIP KSQNFTESGT YYLPSVQIWG SYTNSFKQTF    660
SASNSNLVIG YNATWTDHNV SSSDTVAFGD TSGSALNGHC GPWPYYQCTG TTNGTYSAYH    720
VYITANLRSG NRIGTGGAAN LIFNGVDSIN IANATITQHN AGAYSSSMTF STQNMDNSQN    780
LNGLNSNGKL LVYGTTFTNQ AKDGKFIFNA GQATFENTNF NGGSYQFSGD SLNFSNNNQF    840
NSGSFEIGAK NTIFNNANFN NSTSFNFNNS SATTSFVGDF TNANSNLQIA GNAVFGNSTN    900
GSQNTANFNN TGSVNIAGNA TFDNVVFNSP TNTSVKGKVT LNNITLKNLN APLSFGDGTI    960
VFSAHSVINI GEAITNGNPI TLVSSSKAIE YNDAFSKNLW QLINYQGHGA SSEKLVSSAG   1020
NGVYDVVYSF NNQTYNFQEV FSPNSISIRR LGVGMVFDYV DMEKSDRLYY QNALGFMTYM   1080
PNSYNNNLGN LNNTIYYYDN SIDFYASGKT LFTKAEFSQT FTGQNSAIVF GAKNIWTSVS   1140
DAPQSNVIIR FGDNKGAGSN DASGHCWNLQ CIGFITGHYE AQKIYITGSI ESGNRISSGG   1200
GASLNFNGLQ GILLTNATLY NRAAGTQSSS MNFVSNSANI QAQNSYFIDD TAQNKGNPNF   1260
SFNALNLDFS NSSFRGYVGQ TQSVFKFNAV NAISFTNSSN LSSGLYQMQA KSVLFDNSNL   1320
SVSVGTSSIK ANAINLSQNA SINASNHSTL ELQGDLNLND TSSLNLNQSA INVSNNATIN   1380
DYASLIASNG SHLNFNGAVN FNSANITTSL SSSSIVFKGA VSLRGQFNLS NNSSLDFQGS   1440
SAITSNTAFN FYDNAFSQSP ITFHQALDIK VPLSLGGNLL NPNNSSVLNL KNSQLVFSDQ   1500
GSLNIANIDL LSDLNGNKNR VYNIIQADMN GNWYERINFF GMRINDGIYD AKNQTYSFTN   1560
PLNNALKITE SFKNNQLSVT LSQIPGIKNT LYNIGSEIFN YQKVYNNANG VYSYSDDAQG   1620
VFYLTSSVKG YYNPNQSYQA SGSNNTTKNN NLTSESSVIS QTYNAQGNPI SALHVYNKGY   1680
NFSNIKALGQ MALKLYPEIK KILGNDFSLS SLSNLKGDAL NQLTKLITPS DWKNINELID   1740
NANNSVVQNF NNGTLIIGAT KIGQTDTNSA VVFGGLGYQK PCDYTDIVCQ KFRGTYLGQL   1800
LESISADLGY IDTTFNAKEI YLTGTLGSGN AWGTGGSASV TFNSQTSLIL NQANIVSSQT   1860
DGIFSMLGQE GINKVFNQAG LANILGEVAM QSINKAGGLG NLIVNTLGSD SVIGGYLTPE   1920
QKNQTLSQLL GQNNFDNLMN DSGLNTAIKD LIRQKLGFWT GLVGGLAGLG GIDLQNPEKL   1980
IGSMSINDLL SKKGLFNQIT GFISANDIGQ VISVMLQDIV KPSDALKNDV AALGKQMIGE   2040
FLGQDTLNSL ESLLQNQQIK SVLDKVLAAK GLGSIYEQGL GDLIPNLGKK GIFAPYGLSQ   2100
VWQKGDFSFN AQGNVFVQNS TFSNANGGTL SFNAGNSLIF AGNNHIAFTN HSGTLNLLSN   2160
QVSNINVTML NASNGLKINA TNNNVSVSQG NLFINASCVQ QSDPTTASAT NPCTTAQNNA   2220
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FQANNLTISN QAVLEKNASF VTNNLNIQGA FNNNATQKIE VLQNLVIASN ASLSTGIYGL   2340
EVGGALNNLG AIHFNLENSQ TPVNPLIQVG GIINLNTTQT PFMNVSVANG GTYTLLKSSR   2400
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STLMMETKEN PLFAPIYLEN HSLNEILGVT KDLQNTASLI SNPNFRNNAT SLLEMASYTQ   2580
QTSRLTKLSD FRAREGESNF SERLLELKNK RFSDPNPSEV FVKYSQLSKH PNNLWIQGVG   2640
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LKRNEFTLSA NETYGGNASH INSSNSLLSV LNQRYNYNTW TTSVNGNYGY DFMFKQKSVV 2760
LKPQVGLSYH FIGLSGMKGK MQNPAYQQFV MHSNPSNESV LTLNMGLESR KYFGKNSYYF 2820
VTARLGRDLL IKAKGDNVVR FVGENTLLYR KGEIFNTFAS VITGGEMHLW RLMYVNAGVG 2880
LKMGLQYQDL NITGNVGMRV AF 2902
<212> Type : PRT
<211> Length : 2902
SequenceName : SEQ ID 91
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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KASVLLIGAL GGLSHLRANE CRYWSWSSWS YQDNIESGPN SPTHNSYCLF SSAQGSGTYY 120
LNTLTTYSAG GASFTQKFNG GTLDIGGNIR FGGTGINGGD VGYITGTYNA QTMNFNSSHI 180
TTGNSYADGG GTTLNFNATN NITINQASFD NSDAGTQKSY MNFKGSNIKI SGSSFTDDTN 240
GGFNFSGNNN NSTISFNQTS FNQGTYNFSN SATLSFNNSN FNQGTYHFNS AQSTFENSNF 300
NQGTYNFNDN TSFNNDTFNQ GTYNFNSSKV SFSGANTLNS SSPFASLKGS VSFNSGAIFN 360
LNQTLNNNQT YDILTTNGAI QYGVYQSYLW DLINYKGDKA ISHVEVSNNT YDVTFDINGQ 420
DETLQETFSN QSIITQFLGD DLQQQAQQTY QEDVANSQNA LNKVASDNTI ANNDTSYTQS 480
SNPTILKDAQ GLENTNQQIQ QDEKALEKDL AQIKQLANST TGFNEQAFTQ AQKQEQQDEQ 540
ALQNDENAFN TEQEGLEQAI ANAKHANPTP NPTPSPTPTP IKHTAPNTPP SQVPPTPPSQ 600
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GTLIIGNNTE SVNDNGLIWI GHGGFGYITG TFSAANIYLT NNFKTGEGVS NSDGGGANIT 720
FKASDNITMD GLNYNNAETV TKMIQTGASQ HSYTTFDATN NISVTDSDFS DMTWGKFSFS 780
AKNISFSNAS FSGFTNPGGS STISTNASNS LSFTDSRLNG GAIYNLQANS LIFNNTQAVF 840
NVLYSRGTSN FNATTQLLGN TSFTLSSQSL LNFNGDTTLQ NNANITLGNK SQAAFKNSLT 900
LDNNSNLSLD NQSVLNANGT SAFNNQASLN IYNGSQAAFS SLFFNGGTLS LNANSKLNAS 960
SASFSNNTTI NLDDSVLNAN NTSSLNANIN FQGASQADFG GNTTIDTASF NFDSASSLNF 1020
NNLTANGALN FNGYAPSLTK ALMNVSGQFV LGNNGDINLS DINIFDNITK SVTYNILNAQ 1080
KGITGISGAN GYEKILFYGM KIQNATYSDN NNIQTWSFIN PLNSSQIIQE SIKNGDLTIE 1140
VLNNPNSASN TIFNIAPELY NYQDSKQNPT GYSYDYSDNQ AGTYYLTSNI KGLFTPKGSQ 1200
TPQTPGTYSP FNQPLNSLNI YNKGFSSENL KTLLGILSQN SATLKEMIES NQLDNITNIN 1260
EVLQLLDKIK ITQAQKQALL ETINHLTDNI NQTFNNGNLV IGATQDNVTN STSSIWFGGN 1320
GYSSPCALDS ATCSSFRNTY LGQLLGSTSP YLGYINADFK AKSIYITGTI GSSNAFESGG 1380
SADVTFQSAN NLVLNKANIE AQATDNIFNL LGQEGIDKIF NQGNLANVLS QMAMEKIKQA 1440
GGLGNFIENA LSPLSKELPA SLQDETLGQL IGQNNLDDLL NNSGVMNEIQ NIISQKLSIF 1500
GNFVTPSIIE NYLAKQSLKS MLDDKGLLNF IGGYIDASEL SSILGVILKD ITNPPTSLQK 1560
DIGVVANDLL NEFLGQDVVK KLESQGLVSN IINNVISQGG LSGVYNQGLG SVLPPSLQNA 1620
LKENDLGTLL SPRGLHDFWQ KGYFNFLSNG YVFVNNSSFS NATGGSLNFV ANKSIIFNGD 1680
NTIDFSKYQG ALIFASNGVS NINITTLNAT NGLSLNAGLN NVSVQKGEIC INLANCPTTK 1740
NSSPANSSVT PTNESLSVHA NNFTFLGTII SNGAIDLSQV TNNSVIGTLN LNENATLQAN 1800
NLTITNAFNN ASNSTANIDG NFTLNQQATL STNASGLNVM GNFNSYGDLV FNLSHSVSHA 1860
IINTQGTATI MANNNPLIQF NASSKEVGTY TLIDSAKAIY YGYNNQITGG SSLDNYLKLY 1920
ALIDINGKHM VMTDNGLTYN GQAVSVKDGG LVVGFKDSQN QYIYTSILYN KVKIAVSNDP 1980
INNPQAPTLK QYIAQIQGVQ SVDSIDQAGG NQAINWLNKI FETKGSPLFA PYYLESHSTK 2040
DLTTIAGDIA NTLEVIANPN FKNDATNILQ INTYTQQMSR LAKLSDTSTF ARSDFLERLE 2100
ALKNKRFADA IPNAMDVILK YSQRNRVKNN VWATGVGGAS FISGGTGTLY GINVGYDRFI 2160
KGVIVGGYAA YGYSGFHANI TQSGSSNVNV GVYSRAFIKR SELTMSLNET WGYNKTFINS 2220
YDPLLSIINQ SYRYDTWTTD AKINYGYDFM FKDKSVIFKP QVGLSYYYIG LSGLRGIMDD 2280
PIYNQFRANA DPNKKSVLTI NFALESRHYF NKNSYYFVIA DVGRDLFINS MGDKMVRFIG 2340
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<212> Type : PRT
<211> Length : 2399
SequenceName : SEQ ID 92
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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HYWVKGGQWN KLEVDMKDAV GTYKLSGLRN FTGGDLDVNM QKATLRLGQF NGNSFTSYKD 180
SADRTTRVNF NAKNISIDNF VEINNRVGSG AGRKASSTVL TLQASEGITS SKNAEISLYD 240

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VINPPNNTQK TETEPTQVID GPFAGGKDTV VNIFHLNTKA DGTIKVGGFK ASLTTNAAHL    420
NIGKGGVNLS NQASGRTLLV ENLTGNITVD GPLRVNNQVG GYALAGSSAN FEFKAGVDTK    480
NGTATFNNDI SLGRFVNLKV DAHTANFKGI DTGNGGFNTL DFSGVTDKVN INKLITASTN    540
VAVKNFNINE LIVKTNGISV GEYTHFSEDI GSQSRINTVR LETGTRSIFS GGVKFKSGEK    600
LVINDFYYSP WNYFDARNVK NVEITRKFAS STPENPWGTS KLMFNNLTLG QNAVMDYSQF    660
SNLTIQGDFI NNQGTINYLV RGGKVATLNV GNAAAMMFNN DIDSATGFYK PLIKINSAQD    720
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SGAQGRDLLQ TLLIDSHDAG YARQMIDNTS TGEITKQLNA ATDALNNVAS LEHKQSGLQT    960
LSLSNAMILN SRLVNLSRKH TNHINSFAQR LQALKGQEFA SLESAAEVLY QFAPKYEKPT   1020
NVWANAIGGA SLNSGSNASL YGTSAGVDAF LNGNVEAIVG GFGSYGYSSF SNQANSLNSG   1080
ANNANFGVYS RFFANQHEFD FEAQGALGSD QSSLNFKSTL LQDLNQSYNY LAYSATARAS   1140
YGYDFAFFRN ALVLKPSVGV SYNHLGSTNF KSNSQSQVAL KNGASSQHLF NANANVEARY   1200
YYGDTSYFYL HAGVLQEFAH FGSNDVASLN TFKINAARSP LSTYARAMMG GELQLAKEVF   1260
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<212> Type : PRT
<211> Length : 1288
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      SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
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GYVTQCGGNA NGQKSISSKT IFNNEPGYRS TSITCSLNGH SPGYYGPMSI ENFKKLNEAY    180
QILQTALKRG LPALKENNGK VNVTYTYTCS GDGNNNCSSQ VTGVNNQKDG TKTKIQTIDG    240
KSVTTTISSK VVDSRADGNT TGVSYTEITN KLEGVPDSAQ ALLAQASTLI NTINNACPYF    300
HASNSSEANA PKFSTTTGKI CGAFSEEISA IQKMITDAQE LVNQTSVINE HEQTTPVGNN    360
NGKPFNPFTD ASFAQGMLAN ASAQAKMLNL AEQVGQAINP ERLSGTFQNF VKGFLATCNN    420
PSTAGTGGTQ GSAPGTVTTQ TFASGCAYVG QTITNLKNSI AHFGTQEQQI QQAENIADTL    480
VNFKSRYSEL GNTYNSITTA LSNIPNAQSL QNAVSKKNNP YSPQGIDTNY YLNQNSYNQI    540
QTINQELGRN PFRKVGIVSS QTNNGAMNGI GIQVGYKQFF GQKRKWGARY YGFFDYNHAF    600
IKSSFFNSAS DVWTYGFGAD ALYNFINDKA TNFLGKNNKL SVGLFGGIAL AGTSWLNSEY    660
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<212> Type : PRT
<211> Length : 744
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      SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
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IIGLKGSSDP LKAHSSQITA KLLSNTQSAF DQGIALSSNI ISAVNSLNPS NNSQEVKAQL    180
QNTAQSMAEL LQQIEHSITK TTSTTYAQSL LSNLTDAVNA SSNNTTYVSA LVNALNTLGV    240
GVFPTTTSTH VVLNPPGQVV FYPTNSLLGS TSSNSNNQQQ YNNTLLMNTL QGELSTNNQN    300
NPNGCANQIQ CLEQFIQNLT PLAATPTSTN QANQQVQAIA QKLQSVAINA LDNNAINNTT    360
YNLNNLHNAL NFQAYQSTIE QYNNALKQIS WISFSEPKNL LKNTSNNYQI GTVTNDQGQN    420
ISAYDCTSAT GSLSSDASSG ISCSATSSTN NTNSFDNSLV ATSKVQTING KEQIGVNSFN    480
LVSQVWSVYN SLKTSEENLQ KNAKILCNNG SQSGTSPCNS SSGGLSISGN AQLQNILSPT    540
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NFQQSIQSAF QNQENNIQAW ANALYNTSNP NGNQSQNLTT NNNQDLRIQL RANFYQLINT    660
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GSSGSSSTCS GGLINLLGAI PTNGVSDTNN LINLLTEFIK TAGFIQNKDS NVSTSLTSAF    960
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GLRHYFFFDY GFSEIGLANQ SVKANIFAYG VGTDFLWNLF RRTYNTKALN FGLFAGVQLG 1140
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<211> Length : 1237
SequenceName : SEQ ID 95
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
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NLHQCGSTNS GNGATAAAAT NNSPCFQGNL ALYNEMVDSI KTLSQNISKN IFQGDNNTTS 180
ANLSNQLSEL NTASVYLTYM NSFLNANNQA GGIFQNNTNQ AYENGVTAQQ IAYVLKQASI 240
TMGPSGDSGA AGAFLDAALA QHVFNSANAG NDLSAKEFTS LVQNIVNNSQ NALTLANNAN 300
ISNSTGYQVS YGGNIDQARS TQLLNNTTNT LAKVTALNNE LKANPWLGNF AAGNSSQVNA 360
FNGFITKIGY KQFFGENKNV GLRYYGFFSY NGAGVGNGPT YNQVNLLTYG VGTDVLYNVF 420
SRSFGSRSLN AGFFGGIQLA GDTYISTLRN SPQLASRPTA TKFQFLFDVG LRMNFGILKK 480
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<212> Type : PRT
<211> Length : 527
SequenceName : SEQ ID 96
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
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KALTANGEGI PVLSNTTTKL DFTINGDKRT GGEPNKKLVY PWSHGKAIST SWNATITAPT 240
TENINTTNSA QELLKQASII ITTLNSACPN FQNGGSGYWA GISGNGTMCG MFKNEISAIQ 300
GMIANAQEAV AQAKIVSENT QNQNSLDAGK PFNPYTDASF AESMLKNAQA QAEILNQAEQ 360
VVKNFEKIPT AFVNDSLGVC YEVQGGERRG TNPGQTTSNT WGAGCAYVGQ TITNLKNSIA 420
HFGTQEQQIQ QAENIADTLV NFKSRYSELG NTYNSITTAL SNIPNAQSLQ NAVSKKNNPY 480
SPQGIDTNYY LNQNSYNQIQ TINQELGRNP FRKVGIVSSQ TNNGAMNGIG IQVGYKQFFG 540
QKRKWGARYY GFFDYNHAFI KSSFFNSASD VWTYGFGADA LYNFINDKAT NFLGKNNKLS 600
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<211> Length : 703
SequenceName : SEQ ID 97
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
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FNAMNKALEK NGTATANSTS STSGATGSDG QTYSQQAIQY LQGQQNILNN AANLLKQDEL 240
LLEAFNSAVA ANIGNKEFNS AAFTGLVQGI IDQSQLVYNE LTKNTISGSA VNNAGINSNQ 300
ANAVQGRASQ LPNALYNVQV TLDKINALNN QVRSMPYLPQ FRAGNSRATN ILNGFYTKVG 360
YKQFFGKKRN IGLRYYGFFS YNGASVGFRS TQNNVGLYTY GVGTDVLYNI FSRSYQNRSV 420
DMGFFSGIQL AGETFQSTLR DDPNVKLHGK INNTHFQFLF DFGMRMNFGK LDGKSNRHNQ 480
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<212> Type : PRT
<211> Length : 520
SequenceName : SEQ ID 98
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
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SYAISPCGPG KDTSKNGGVQ TFHNTPSNQW GGTTITCGTT GYEPGPYSIL STENYAKINK 180
AYQIIQKAFG SSGKDIPALS DTNTELKFTI NKNNGNTNTN NNGEEIVTKN NAQVLLEQAS 240
TIITTLNSAC PWINNGGAGG ASSGSLWEGI YLKGDGSACG IFKNEISAIQ DMIKNAAIAV 300
EQSKIVAANA QNQRNLDTGK TFNPYKDANF AQSMFANAKA QAEILNRAQA VVKDFERIPA 360
EFVKDSLGVC HEVQNGHLRG TPSGTVTDNT WGAGCAYVGE TVTNLKDSIA HFGDQAERIH 420
NARNLAYTLA NFSSQYQKLG EHYDSITAAI SSLPDAQSLQ NVVSKKTNPN SPQGIQDNYY 480
IDSNIHSQVQ SRSQELGSNP FRRAGLIAAS TTNNGAMNGI GFQVGYKQFF GKNKRWGARY 540
YGFVDYNHTY NKSQFFNASS DVWTYGVGSD LLVNFINDKA TKHNKISFGA FGGIALAGTS 600
WLNSQYVNLA NVNNYYKAKI NTANFQFLFN LGLRMNLARK KHRATDNAAQ HGIELGTKIP 660
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<212> Type : PRT
<211> Length : 690
SequenceName : SEQ ID 99
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
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IAFGISCGPG PNLGPEHLEN GGVRSFDNTP NYSYNTGSGT TTTTCNGASN VGPNGILSSS 180
EYQVLNTAYQ TIQTALNQNQ GGGMPALNSS KNMVVNINQT FTKNPTTEYT YPDGNGNYYS 240
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SFNAINEMIK NAQAVLEKTQ QLNANENTQI TQPDNFNPYT SKDTQFAQEM LNRANAQAEI 360
LSLAQQVADN FHSIQGPIQQ DLEECTAGSA GVINDNTYGS GCAFVKETLN SLEQHTAYYG 420
NQVNQDRALS QTILNFKEAL STLGNDSKAI NSGISNLPNA KSLQNMTHAT QNPNSPEGLL 480
TYSLDTSKYN QLQTVAQELG KNPFRRIGVI NYQNNNGAMN GIGVQAGYKQ FFGKKRNWGL 540
RYYGFFDYNH AYIKSNFFNS ASDVWTYGVG MDALYNFIND KNTNFLGKNN KLSVGLFGGF 600
ALAGTSWLNS QQVNLTMMNG IYNANVSASN FQFLFDLGLR MNLARPKKKD SDHAAQHGME 660
LGVKIPTINT DYYSFMGAEL KYRRLYSVYL NYVFAY 696
<212> Type : PRT
<211> Length : 696
SequenceName : SEQ ID 100
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
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LNQYNYLNSL VNLASTPSAI TGAIDNLSSS AINLTSATTT SPAYQAVALA LNAAVGMWQV 120
IAFGISCGPG PNLGPEHLEN GGVRSFDNTP NYSYNTGSGT TTTTCNGASN VGPNGILSSS 180
EYQVLNTAYQ TIQTALNQNQ GGGMPALNSS KNMVVNINQT FTKNPTTEYT YPDGNGNYYS 240
GGSSIPIQLK ISSVNDAENL LQQAATIINV LTTQNPHVNG GGGAWGFGGK TGNVMDIFGD 300
SFNAINEMIK NAQAVLEKTQ QLNANENTQI TQPDNFNPYT SKDTQFAQEM LNRANAQAEI 360
LSLAQQVADN FHSIQGPIQQ DLEECTAGSA GVINDNTYGS GCAFVKETLN SLEQHTAYYG 420
NQVNQDRALS QTILNFKEAL STLGNDSKAI NSGISNLPNA KSLQNMTHAT QNPNSPEGLL 480
TYSLDTSKYN QLQTVAQELG KNPFRRIGVI NYQNNNGAMN GIGVQAGYKQ FFGKKRNWGL 540
RYYGFFDYNH AYIKSNFFNS ASDVWTYGVG MDALYNFIND KNTNFLGKNN KLSVGLFGGF 600
ALAGTSWLNS QQVNLTMMNG IYNANVSASN FQFLFDLGLR MNLARPKKKD SDHAAQHGME 660
LGVKIPTINT DYYSFMGAEL KYRRLYSVYL NYVFAY 696
<212> Type : PRT
<211> Length : 696
SequenceName : SEQ ID 101
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
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DEEVKKYTGS RTVISNKALT QQANQSIEEA LQNVPGLQIR NATGVGAMPT IQIRGFGAGG 120

SGHSDATLML VNGIPVYMAP YAHIELDIFP VTFQAIDRID VIKGGGSVQY GPNTYGGIVN 180
IITKPIPNQW ENQAAERITY WAKARNAGFA APPDKTGDPS FIKSLGNNLL YNTYVRSGGM 240
INKHVGIQAQ ANWVRGQGFR DNSPSSISNY WLDGVYDINE SNGIKAYYQY YDFAIAQPGS 300
LSEQDYKINR FANLRPLNQK GGRSQRFGAV YENRFGDLDR VGGTFSFTYY GQLMTRDFQV 360
SSSYNSANMV TCFSEAACRA AGLPAGYNLA VPYYATNYNG WAEVENPVRS INNAFEPKVN 420
LIVNTGKVRQ TFIMGLRFMT TTFLQRQYLN TNECATKTSG EGAGFLCEGP NVMSGWKPHI 480
KHGVYRNWNN WRNNYTAVYL SDRIEAWDGR FFIVPGLRYA FVQYNNENAS NWMQIPEKDL 540
RKIKHMNNWM PSTNIGFIPV QGDHNVLTYF NYQRSFVPPQ LDVLSYGGAE YFTQHFDTVE 600
AGARYTYKDK FSFNADYFRI WARDFATGQY SVYTSGPMKG NVRPINGYSQ GVELELYYRP 660
IRGLQFHAAF NYIDTRVTSH GPLTDLNGDV LKGTSYNKHF PFVSPFQFIF DARYNWRKTT 720
IGISSYFYSR AYSGISNSAA GGYYGMQYYS GGNNYESVLN SGYQCEAWCM TQHEGLLPWY 780
WVWNIQVSQI FWENGRHRVT GSLQINNIFN MKYYFTGIGS SPAGLQPAPG RSVTAYLNYT 840
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<212> Type : PRT
<211> Length : 841
SequenceName : SEQ ID 102
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
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VQCGPGNSGQ QSVTFEGQPG HNSSSINCNL TGYNNGVSGP LSIENFKKLN QAYQTIQQAL 180
KQDSGFPVLD SAGKQVTITI TTQTNGANKS ETTTTTTTTN DAQTLLQEAS KMISVLTTNC 240
PWVNHNQGQN GGAPWGLDTA GNVCQVFATE FSAVTSMIKN AQEIVTQAQS LNQQNNQNAP 300
QDFNPYTSAD RAFAQNMLNH AQAQAKILEL ADQMKKDLNT IPSQFITNYL AACHNGGGTL 360
PDAGVTNNTW GAGCAYVEET ITALNNSLAH FGTQAEQIKQ SELLARTILD FRGSLSNLNN 420
TYNSITTTAS NTPNSPFLKN LISQSTNPNN PGGLQAVYQV NQSAYSQLLS ATQELGHNPF 480
RRVGLISSQT NNGAMNGIGV QVGYKQFFGE KRRWGLRYYG FFDYNHAYIK SSFFNSASDV 540
FTYGVGTDVL YNFINDKTTK NSKISFGVFG GIALAGTSWL NSQYVNLATF NNFYSAKMNV 600
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YLNYVFAY 668
<212> Type : PRT
<211> Length : 668
SequenceName : SEQ ID 103
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
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IDLGVIETIP KHSKIVLPGE AFDSLKEAFD KIDPYTLFLP KFEATSTSIS DTNTQRVFET 180
LNNIKTNLIM KYSNENPNNF NTCPYNNNGN TKNDCWQNFT PQTAEEFTNL MLNMIAVLDS 240
QSWGDAILNA PFEFTNSSTD CDSDPSKCVN PGVNGRVDTK VDQQYILNKQ GIINNFRKKI 300
EIDAVVLKNS GVVGLANGYG NDGEYGTLGV EAYALDPKKL FGNDLKTINL EDLRTILHEF 360
SHTKGYGHNG NMTYQRVPVT KDGQVEKDSN GKPKDSDGLP YNVCSLYGGS NQPAFPSNYP 420
NSIYHNCADV PAGFLGVTAA VWQQLINQNA LPINYANLGS QTNYNLNASL NTQDLANSML 480
STIQKTFVTS SVTNHHFSNA SQSFRSPILG VNAKIGYQNY FNDFIGLAYY GIIKYNYAKA 540
VNQKVQQLSY GGGIDLLLDF ITTYSNKNSP TGIQTKRNFS SSFGIFGGLR GLYNSYYVLN 600
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<212> Type : PRT
<211> Length : 668
SequenceName : SEQ ID 104
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
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AFNSPKMFLG LEFGLGIAGA TYMPGGAMHG IIAQYLGKEN SLFQLLVKVG FRFGFFHNEI 180

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<211> Length : 220
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SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
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VVCGGYIKKP GENNQKNFHY TDENGNGTTI NCGGSTNSNG THSPNGTNTL KADKNVSLSI 180
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LANQVASDFD KLSSGYLKDY IGKCDVSGVS SSNMTPQNMN TTWGKGCAGV EETLTSLKAS 420
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QKRRWGLRYY GFFDYNHTYI KSSFFNSSSD VLTYGVGSDL LFNFINDKNT NFLGKNNKIS 540
VGLFGGIALA GTSWLNSQFV NLKTISNVYS AKVNTANFQF LFNLGLRTNL ARPKKKDSDH 600
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<211> Length : 643
SequenceName : SEQ ID 106
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
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FGHNPFRSVG LINSQSNNGA MNGVGVQLGY KQFFGKNKFF GIRYYGFFDY NYAYIKSNFF 360
NSASNVFTYG AGSDLLLNFI NGGSDRNRKV SFGIFGGIAL AGTTWLNNQS ANLKITNSAY 420
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<212> Type : PRT
<211> Length : 483
SequenceName : SEQ ID 107
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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QTDSLETQNM KHNKNVRNYV FSDAYLEYAY KNYFEIKAGR YLSTMPYKSG QTQGFQVSGQ 180
YKHARLTWFS SWGRAFAYGS FLMDWFAART TYSGGFTKNN NGGYDSHGRK VLYGTHAVQL 240
TYKPHRFLIE GFYYLSPQIF NAPGVKIGWD SNPNFSGTGF RSDTAIIGFF PIYYPWMIVK 300
SNGSPVYRYD TPATQNGQNL IIRQRFDINN YNVSIAFYKV FQNANGWIGN MGNPSGVIMG 360
SNSVYAGFTG TALKRDAATI FLSCGGTHFA KKFTWKFATQ YSNSVVSWEA RAMISLGYKF 420
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<212> Type : PRT
<211> Length : 471
SequenceName : SEQ ID 108
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MLRLVSKTIC LSLISLFNPL EAFQKHQKDV FFVEAGFETG LLEGAQTKEQ AIAQNTQNTQ 60

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KIYENPLTHP QTKEQPKEQN KSDTATPQSV YGRYYILQNT ILEKATELFT AANINGNGLT     120
FYSQNPVYVM AYNKDNAEFE GYGNNSVVVI QNFLPYNLNN IELSYTDAQG KAVNLGVIET     180
IPKDSQIILP ASLFNNFSND SPFNSDGLQQ LQTTTTPFSD ANTQSLFEKL SQITTNLQMT     240
YENTDPFSSG NNDPNGPLAS PKPHYECPGY KKSCQVASVS FTPQTAEELT NLMLDMIAVF     300
DSKSWEEAVL NAPFQFSNSP SECGIDYPKC VNPFNNGLVD PKDEKYALTP EEVINSYRVA     360
NELTVNLLNA AKGFLGLGSQ LGSANAPDDD GFNQGVLGIA PFALDPEKLF GKNLNKVAIL     420
ALRDIIHEYG HTLGYTHNGN MTYQRVRLCQ EGNGPEARCE GGHEVEKNGK EELEFSNGHE     480
VRDHDGYTYD VCSRFGGKNQ PAFPSNYPNS IYTNCAQVPA GLIGVTTAVW QQLINQNALP     540
INFANLNSQT SHLNAGLNAQ NFATSMVSAI AQNFSTTSTT TYRSSSKNFR SPILGVNVKI     600
GYQHYFNDYI GLAYYGIIQY NYAQANDEKI QQLSYGGGMD VLFDFITTYT NKKQDHPTKK     660
VFASSFGVFG GLRGLYNSYY VFNQVKGSGN LDIVTGFNYR YKHSKYSIGV SVPLIQSGIK     720
IASNNGIYAD SVVLNEGGSH FKVFFNYGWV F                                    751
<212> Type : PRT
<211> Length : 751
      SequenceName : SEQ ID 109
      SequenceDescription :

Sequence
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<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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YIRQNAIALE SAAVPLAYYL EAMGQQTRVL MQMLCPDPSK RCLLYAGGYQ NGQNNNGDTG     120
NNPPRGNVNA TFDMQSLVNN LNKLTQLIGE TLIRNPENLP NSKVFNVKFG NQSTVIALPE     180
GLANTMDALN NDITNALTTL WYNQTLTNKS FSTPSNTSVN FSPQVLQHLL QDGLATANNN     240
QTICSTQNQC TATNEAKSIA QNAQNIFQAL MQAGILGGLA NEKQFGFTYN KAPNGSDSQQ     300
GYQSFSGPGY YTKNDNTTQA PLKALPAGAT IGSGNGQYTY HPSSAVYYLA DSIIANGITA     360
SMIFSGMQNF ANKAAKLIGT SSYNQMQDAI NYGESLLSNT VAYGDFITNW VAPYLDLNNK     420
GLNFLPNYGG QLNGANNQTP QLTPQQAQQE QKVIMNQLEQ ATNAPTPAQI NRILANPYSP     480
TAKTLMAYGL YRSKAVIGGV IDEMQTKVNQ VYQMGFARNF LEHNSNSNNM NGFGVKMGYK     540
QFFGKKRMFG LRYYGFYDFG YAQFGTESSL VKATLSSYGA GTDFLYNVFT RKRGTEAIDI     600
GFFAGIQLAG QTWKTNFLDQ VDGNHLKPKD TSFQFLFDLG IRTNFSKIAH QKRSRFSQGI     660
EFGLKIPVLY HTYYQSEGVT AKYRRDFSFY VGYNIGF                              697
<212> Type : PRT
<211> Length : 697
      SequenceName : SEQ ID 110
      SequenceDescription :

Sequence
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<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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AGNYLTFFVV NKDTQKPASV QGNPPFSTIV QNCSGIENCA MNQTTYDKMK KLAEDLQAAQ     180
QNATTKANNL CALSGCATTQ GQNPSSTVSN ALNLAQQLMD LIANTKTAMM WKNIVIAGVS     240
NVSGAIDSTG YPTQYAVFNN IKAMIPILQQ AVTLSQSNHT LSASLQAQAT GSQTNPKFAK     300
DIYAFAQNQK QVISYAQDIF NLFSSIPKDQ YRYLEKAYLK IPNAGKTPTN PYRQEVNLNQ     360
EIQTIQNNVS YYGNRVDAAL SVAKDVYNLK SNQTEIVTTY NNAKNLSQEI SKLPYNQVNT     420
KDIITLPYDQ NAPAAGQYNY QINPEQQSNL SQALAAMSNN PFKKVGMISS QNNNGALNGL     480
GVQVGYKQFF GESKRWGLRY YGFFDYNHGY IKSSFFNSSS DIWTYGGGSD LLVNFINDSI     540
TRKNNKLSVG LFGGIQLAGT TWLNSQYMNL TAFNNPYSAK VNASNFQFLF NLGLRTNLAT     600
AKKKDSERSA QHGVELGIKI PTINTNYYSF LGTKLEYRRL YSVYLNYVFA Y              651

<212> Type : PRT
<211> Length : 651
      SequenceName : SEQ ID 111
      SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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PKPKPKPITP QSTYGKYYIS QSTILKNATE LFAEDNITNL TFYSQNPVYV TAYNQESAEE     120
AGYGNNSLIM IQNFLPYNLN NIELSYTDDQ GNVVSLGVIE TIPKQSQIIL PASLFNDPQL     180
NADGFQQLQT NTTRFSDAST QNLFNKLSKV TTNLQMTYIN YNQFSSGNGS GSKPPCPPYE     240
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NQANCVAKVP PFTSQDAKNL TNLMLNMMAV FDSKSWEDAV LNAPFQFSDN NLSAPCYSDY 300
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GGDLGLGSQY GGPNGPGDDG TNFGALGILS PFLDPEILFG KELNKVAIMQ LRDIIHEYGH 420
TLGYTHNGNM TYQRVRMCEE NNGPEERCQG GRIEQVDGKE VQVFDNGHEV RDTDGSTYDV 480
CSRFKDKPYT AGSYPNSIYT DCSQVPAGLI GVTSAVWQQL IDQNALPVDF TNLSSQTNYL 540
NASLNTQDFA TTMLSAISQS LSSSKSSATT YRTSKTSRPF GAPLLGVNLK MGYQKYFNDY 600
LGLSSYGIIK YNYAQANNEK IQQLSYGVGM DVLFDFITNY TNEKNPKSNL TKKVFTSSLG 660
VFGGLRGLYN SYYLLNQYKG SGNLNVTGGL NYRYKHSKYS IGISVPLVQL KSRIVSSDGA 720
YTNSITLNEG GSHFKVFFNY GWIF 744
<212> Type : PRT
<211> Length : 744
SequenceName : SEQ ID 112
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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IDLGVIETIP KHSKIVLPGE AFDSLKIDPY TLFLPKIEAT STSISDANTQ RVFETLNKIK 180
TNLVVNYRNE NKFKDHENHW EAFTPQTAEE FTNLMLNMIA VLDSQSWGDA ILNAPFEFTN 240
SPTDCDNDPS KCVNPGTNGL VNSKVDQKYV LNKQDIVNKF KNKADLDVIV LKDSGVVGLG 300
SDITPSNNDD GKHYGQLGVV ASALDPKKLF GDNLKTINLE DLRTILHEFS HTKGYGHNGN 360
MTYQRVPVTK DGQVEKDSNG KPKDSDGLPY NVCSLYGGSN QPAFPSNYPN SIYHNCADVP 420
AGFLGVTAAV WQQLINQNAL PINYANLGSQ TNYNLNASLN TQDLANSMLS TIQKTFVTSS 480
VTNHHFSNAS QSFRSPILGV NAKIGYQNYF NDFIGLAYYG IIKYNYAKAV NQKVQQLSYG 540
GGIDLLLDFI TTYSNKNSPT GIQTKRNFSS SFGIFGGLRG LYNSYYVLNK VKGSGNLDVA 600
TGLNYRYKHS KYSVGISIPL IQRKASVVSS GGDYTNSFVF NEGASHFKVF FNYGWVF 657

<212> Type : PRT
<211> Length : 657
SequenceName : SEQ ID 113
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MSLATSYNVS NNFSKFNIKR VRGYLICLVC NTPKMIQRGL NGVSFYGCSD YVNKGDCKGV 60
LREINGSMKM VCLHCENTPI MEKVESGRGG AYACKNCNRK FYFIDLAKQN ERKKDLEKEK 120
KELLNKIEKQ KIKHLERFIL AGVKANIKEN SFFLGCKNYP KCEWTASMDS QDLKCPKCNR 180
LMKRKKNFKN NEFFTATSLT LNAIEFCLYI NLKKKETNV 219
<212> Type : PRT
<211> Length : 219
SequenceName : SEQ ID 114
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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SYTSLLGELN LSMGLYKGLR AEVGAMMAAL PYDSTAYQGN NIPNGQPGSR TDPFGAGIFW 120
QYIGWYAGHS GLNVQKPRLA MVHNAFLSYN YKKDKFSFGV KGGRYDAEEY DWFTSYTQGV 180
EGFVKYKDTR LRVMYSDARA SASSDWFWYF GRYYTSGKAL MIADLKYEKD NLKINPYFYA 240
IFQRMYAPGI NITYDTNPNF NNKGFRFVGT FVGFFPIFAT PANQNDIILF QQVPLGKSGQ 300
TYFFRTRFYY NKWQFGGSVY KNIGNANGDI GIYGDPLGYN IWTNSIYDAE INNIVGADVI 360
NGFLYVGSQY RGFSWKILGR WTDSPRADER SLALFLSYFS NKYNIRMDLK LEYYGNITKK 420
GYCIGYCGMY VPVDPNGPGT QPLTHNVYSD RSHIMFNITY GFRIY 465
<212> Type : PRT
<211> Length : 465
SequenceName : SEQ ID 115
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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AQLASLKKSI QTANNIQAVN NALSDLKSFA SNNHTNKETS PIYNTAQAVI TSVLAFWSLY 120
AGNALSFHVT GLNDGSNSPL GRIHRDGNCT GLQQCFMSKE TYDKMKTLAE NLQKAQGNLC 180
ALSECSSNQS NGGKTSMTTA LQTAQQLMDL IEQTKVSMVW KNIVIAGVTN KPNGAGAITS 240
TGHVTDYAVF NNIKAMLPIL QQALTLSQSN HTLSTQLQAR AMGSQTNREF AKDIYALAQN 300
QKQILSNASS IFNLFNSIPK DQLKYLENAY LKVPHLGKTP TNPYRQNVNL NKEINAVQDN 360
VANYGNRLDS ALSVAKDVYN LKSNQTEIVT TYNDAKNLSE EISKLPYNQV NVTNIVMSPK 420
DSTAGQYQIN PEQQSNLNQA LAAMSNNPFK KVGMISSQNN NGALNGLGVQ VGYKQFFGES 480
KRWGLRYYGF FDYNHGYIKS SFFNSSSDIW TYGGGSDLLV NFINDSITRK NNKLSVGLFG 540
GIQLAGTTWL NSQYMNLTAF NNPYSAKVNA SNFQFLFNLG LRTNLATAKK KDSERSAQHG 600
VELGIKIPTI NTNYYSFLGT KLEYRRLYSV YLNYVFAY 638
<212> Type : PRT
<211> Length : 638
SequenceName : SEQ ID 116
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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ETFVNLTGKL EGSVHLGRGW TVNVGGVLGG QVYDNTRYDR WAKDFTPPSY WDKTSCGTDS 120
LSLCMNATKM WQQQGPGGII DPRGIGYMYM GEWNGLFPNY YPANAYLPGH SRRYEVYKAN 180
LTYDSDRVHM VMGRFDVTEQ EQMDWIYQLF QGFYGTFKLT KNMKFLLFSS WGRGIADGQW 240
LFPIYREKPW GIHKAGIIYR PTKNLMIHPY VYLIPMVGTL PGAKIEYDTN PEFSGRGIRN 300
KTTFYVLYDY RWNNAEYGRY APARYNTWDP FLDNGKWRGL QGPGGATLYL HHHIDINNYF 360
VVGGAYLNIG NPNMNLGTWG NPVALDGIEQ WVGGIYSLGF AGIDNITDAD AFTEYVKGGG 420
KHGKFSWSVY QRFTTAPRAL EYGIGMYLDY QFSKHVKAGL KLVWLEFQIR AGYNPGTGFL 480
GPNGQPLNLN NGLFESSAFA QGPQNMGGIA KSITQDRSHL MTHISYSF 528
<212> Type : PRT
<211> Length : 528
SequenceName : SEQ ID 117
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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NPANMGFTND WGENRSEFEM TTTVINIPAF SFKVPTTNQG LYSVTSLEID KSQQNILGII 120
NTIGLGNILK ALGNTAATNG LSQAINRVQG LMNLTNQKVV TLASKPDTQI VNGWTGTTNF 180
VLPKFFYKTR THNGFTFGGS FTAPSGLGMK WNGKGGEFLH DVFIMMVELA PSMSYTINKR 240
FSVGVGLRGL YATGSFNNTV YVPLEGASVL SAEQILNLPN NVFADQVPSN MMTLLGNIGY 300
QPALNCQKAG GDMSDQSCQE FYNGLKKIMG YSGLIKASAN LYGTTQVVQK SNGQGVSGGY 360
RVGSSLRVFD HGMFSVVYNS SVTFNMKGGL VAITELGPSL GSVLTKGSLN INVSLPQTLS 420
LAYAHQFFKD RLRVEGVFER TFWSQGNKFL VTPDFANATY KGLSGTVASL DSETLKKMVG 480
LANFKSVMNM GAGWRDTNTF RLGVTYMGKS LRLMGAIDYD QAPSPQDAIG IPDSNGYTVA 540
FGTKYNFRGF DLGVAGSFTF KSNRSSLYQS PTIGQLRIFS ASLGYRW 587
<212> Type : PRT
<211> Length : 587
SequenceName : SEQ ID 118
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MAFQVNTNIN AMNAHVQSAL TQNALKTSLE RLSSGLRINK AADDASGMTV ADSLRSQASS 60
LGQAIANTND GMGIIQVADK AMDEQLKILD TVKVKATQAA QDGQTTESRK AIQSDIVRLI 120
QGLDNIGNTT TYNGQALLSG QFTNKEFQVG AYSNQSIKAS IGSTTSDKIG QVRIATGALI 180
TASGDISLTF KQVDGVNDVT LESVKVSSSA GTGIGVLAEV INKNSNRTGV KAYASVITTS 240
DVAVQSGSLS NLTLNGIHLG NIADIKKNDS DGRLVAAINA VTSETGVEAY TDQKGRLNLR 300
SIDGRGIEIK TDSVSNGPSA LTMVNGGQDL TKGSTNYGRL SLTRLDAKSI NVVSASDSQH 360
LGFTAIGFGE SQVAETTVNL RDVTGNFNAN VKSASGANYN AVIASGNQSL GSGVTTLRGA 420
MVVIDIAESA MKMLDKVRSD LGSVQNQMIS TVNNISITQV NVKAAESQIR DVDFAEESAN 480

FNKNNILAQS GSYAMSQANT VQQNILRLLT 510
<212> Type : PRT
<211> Length : 510
SequenceName : SEQ ID 119
SequenceDescription :

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<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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MTQYNQSIAE AVSVPMKAAN QQYNQLYQGF NDQSMAVGNN ILNISKLTGE FNAQGNTQSA 120
QISAVNSQIA SILASNTTPK NPSAIEAYAT NQIAVPSVPT TVEMMSGILG NITSAAPKYA 180
LALQEQLRSQ ASNSSMNDTA DSLDSCTALG ALVGSSKVFF SCMQISMTPM SVSMPTVYAK 240
YQAVATKALT SGVNPMTTPA CPIGDKVLAV YCYAEKVAEI LREYYIEFVK NNTNLLQNAS 300
QMILNQSGLA TSTYDTQAIS NISSLYNYNI VANKSFLKSH LTYLDYIKDK LKGQKDSYLT 360
ERVQTKIIVK 370
<212> Type : PRT
<211> Length : 370
SequenceName : SEQ ID 120
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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ISQLREEFAN KAIKNPTKKN QYFSSFISKS NDLIDKDNLI DTGSSIKSFQ KFGTQRYQIF 120
MNWVSHQNDP SKINTQKIRG FMENIIQPPI SDDKEKAEFL RSAKQAFAGI IIGNQIRSDQ 180
KFMGVFDESL KERQEAEKNG EPNGDPTGGD WLDIFLSFVF NKKQSSDLKE TLNQEPVPHV 240
QPDVATTTTD IQSLPPEARD LLDERGNFSK FTLGDMNMLD VEGVADIDPN YKFNQLLIHN 300
NALSSVLMGS HNGIEPEKVS LLYGNNGGPE ARHDWNATVG YKNQRGDNVA TLINVHMKNG 360
SGLVIAGGEK GINNPSFYLY KEDQLTGSQR ALSQEEIQNK VDFMEFLAQN NAKLDNLSKK 420
EKEKFQNEIE DFQKDSKAYL DALGNDHIAF VSKKDKKHLA LVAEFGNGEL SYTLKDYGKK 480
ADKALDREAK TTLQGSLKHD GVMFVDYSNF KYTNASKSPD KGVGATNGVS HLEAGFSKVA 540
VFNLPNLNNL AITSVVRQDL EDKLIAKGLS PQEANKLVKD FLSSNKELVG KALNFNKAVA 600
EAKNTGNYDE VKQAQKDLEK SLKKRERLEK DVAKNLESKS GNKNKMEAKS QANSQKDEIF 660
ALINKEANRD ARAIAYAQNL KGIKRELSDK LENINKDLKD FSKSFDEFKN GKNKDFSKAE 720
ETLKALKGSV KDLGINPEWI SKVENLNAAL NEFKNGKNKD FSKVTQAKSD LENSIKDVII 780
NQKITDKVDN LNQAVSVAKA TGDFSGVEQA LADLKNFSKE QLAQQAQKNE DFNTGKNSAL 840
YQSVKNGVNG TLVGNGLSKA EATTLSKNFS DIKKELNAKL GNFNNNNNNG LENSTEPIYT 900
QVAKKVKAKI DRLDQIASGL GDVGQAASFL LKRHDKVDDL SKVGLSANHE PIYATIDDLG 960
GPFPLKRHDK VDDLSKVGLS REQKLTQKID NLNQAVSEAK ASHFDNLDQM IDKLKDSTKK 1020
NVVNLYVESA KKVPTSLSAK LDNYATNSHT RINSNVKNGT INEKATGMLT QKNSEWLKLV 1080
NDKIVAHNVG SAPLSAYDKI GFNQKNMKDY SDSFKFSTRL SNAVKDIKSG FVQFLTNIFS 1140
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<212> Type : PRT
<211> Length : 1167
SequenceName : SEQ ID 121
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
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LRPAFQYSDN IAKEYENKFK NQTTLKVEEI LQNQGYKVIN VDSSDKDDFS FAQKKEGYLA 120
VAMNGEIVLR PDPKRTIQKK SEPGLLFSTG LDKMEGVLIP AGFVKVTILE PMSGESLDSF 180
TMDLSELDIQ EKFLKTTHSS HSGGLVSTMV KGTDNSNDAI KSALNKIFAS IMQEMDKKLT 240
QRNLESYQKD AKELKNKRNR 260
<212> Type : PRT
<211> Length : 260
SequenceName : SEQ ID 122
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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SYELVDWKRV GDTKLVALVR SALVRVKFQD TTSSDQSNTN QNALSFDTQE SQKALNGSQS 120
GSSDTSGSNS QDFASYVLIF KAAPRATWVF ERKIKLALPY VKQESQGSGD QGSNGKGSLY 180
KTLQDLLVEQ PVTPYTPNAG LARVNGVAQD TVHFGSGQES SWNSQRSQKG LKNNPGPKAV 240
TGFKLDKGRA YRKLNESWPV YEPLDSTKEG KGKDESSWKN SEKTTAENDA PLVGMVGSGA 300
AGSASSLQGN GSNSSGLKSL LRSAPVSVPP SSTSNQTLSL SNPAPVGPQA VVSQPAGGAT 360
AAVSVNRTAS DTATFSKYLN TAQALHQMGV IVPGLEKWGG NNGTGVVASR QDATSTNLPH 420
AAGASQTGLG TGSPREPALT ATSQRAVTVV AGPLRAGNSS ETDALPNVIT QLYHTSTAQL 480
AYLNGQIVVM GSDRVPSLWY WVVGEDQESG KATWWAKTEL NWGTDKQKQF VENQLGFKDD 540
SNSDSKNSNL KAQGLTQPAY LIAGLDVVAD HLVFAAFKAG AVGYDMTTDS SASTYNQALA 600
WSTTAGLDSD GGYKALVENT AGLNGPINGL FTLLDTFAYV TPVSGMKGGS QNNEEVQTTY 660
PVKSDQKATA KIASLINASP LNSYGDDGVT VFDALGLNFN FKLNEERLPS RTDQLLVYGI 720
VNESELKSAR ENAQSTSDDN SNTKVKWTNT ASHYLPVPYY YSANFPEAGN RRRAEQRNGV 780
KISTLESQAT DGFANSLLNF GTGLKAGVDP APVARGHKPN YSAVLLVRGG VVRLNFNPDT 840
DKLLDSTDKN SEPISFSYTP FGSAESAVDL TTLKDVTYIA ESGLWFYTFD NGEKPTYDGK 900
QQQVKNRKGY AVITVSRTGI EFNEDANTTT LSQAPAALAV QNGIASSQDD LTGILPLSDE 960
FSAVITKDQT WTGKVDIYKN TNGLFEKDDQ LSENVKRRDN GLVPIYNEGI VDIWGRVDFA 1020
ANSVLQARNL TDKTVDEVIN NPDILQSFFK FTPAFDNQRA MLVGEKTSDT TLTVKPKIEY 1080
LDGNFYGEDS KIAGIPLNID FPSRIFAGFA ALPSWVIPVS VGSSVGILLI LLILGLGIGI 1140
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KPAAPTAPRP PVQPPKKA 1218
<212> Type : PRT
<211> Length : 1218
SequenceName : SEQ ID 123
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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AINPRLTPWT YRNTSFSSLP LTGENPGAWA LVRDNSAKGI TAGSGSQQTT YDPTRTEAAL 120
TASTTFALRR YDLAGRALYD LDFSKLNPQT PTRDQTGQIT FNPFGGFGLS GAAPQQWNEV 180
KNKVPVEVAQ DPSNPYRFAV LLVPRSVVYY EQLQRGLGLP QQRTESGQNT STTGAMFGLK 240
VKNAEADTAK SNEKLQGAEA TGSSTTSGSG QSTQRGGSSG DTKVKALKIE VKKKSDSEDN 300
GQLQLEKNDL ANAPIKRSEE SGQSVQLKAD DFGTALSSSG SGGNSNPGSP TPWRPWLATE 360
QIHKDLPKWS ASILILYDAP YARNRTAIDR VDHLDPKAMT ANYPPSWRTP KWNHHGLWDW 420
KARDVLLQTT GFFNPRRHPE WFDGGQTVAD NEKTGFDVDN SENTKQGFQK EADSDKSAPI 480
ALPFEAYFAN IGNLTWFGQA LLVFGGNGHV TKSAHTAPLS IGVFRVRYNA TGTSATVTGW 540
PYALLFSGMV NKQTDGLKDL PFNNNRWFEY VPRMAVAGAK FVGRELVLAG TITMGDTATV 600
PRLLYDELES NLNLVAQGQG LLREDLQLFT PYGWANRPDL PIGAWSSSSS SSHNAPYYFH 660
NNPDWQDRPI QNVVDAFIKP WEDKNGKDDA KYIYPYRYSG MWAWQVYNWS NKLTDQPLSA 720
DFVNENAYQP NSLFAAILNP ELLAALPDKV KYGKENEFAA NEYERFNQKL TVAPTQGTNW 780
SHFSPTLSRF STGFNLVGSV LDQVLDYVPW IGNGYRYGNN HRGVDDITAP QTSAGSSSGI 840
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DKASSGQSDE NHTKFTSATG MDQQGQSGTS AGNPDSLKQD NISKSGDSLT TQDGNAIDQQ 960
EATNYTNLPP NLTPTADWPN ALSFTNKNNA QRAQLFLRGL LGSIPVLVNR SGSDSNKFQA 1020
TDQKWSYTDL HSDQTKLNLP AYGEVNGLLN PALVETYFGN TRAGGSGSNT TSSPGIGFKI 1080
PEQNNDSKAT LITPGLAWTP QDVGNLVVSG TTVSFQLGGW LVTFTDFVKP RAGYLGLQLT 1140
GLDASDATQR ALIWAPRPWA AFRGSWVNRL GRVESVWDLK GVWADQAQSD SQGSTTTATR 1200
NALPEHPNAL AFQVSVVEAS AYKPNTSSGQ TQSTNSSPYL HLVKPKKVTQ SDKLDDDLKN 1260
LLDPNQVRTK LRQSFGTDHS TQPQPQSLKT TTPVFGTSSG NLSSVLSGGG AGGGSSGSGQ 1320
SGVDLSPVEK VSGWLVGQLP STSDGNTSST NNLAPNTNTG NDVVGVGRLS ESNAAKMNDD 1380
VDGIVRTPLA ELLDGEGQTA DTGPQSVKFK SPDQIDFNRL FTHPVTDLFD PVTMLVYDQY 1440
IPLFIDIPAS VNPKMVRLKV LSFDTNEQSL GLRLEFFKPD QDTQPNNNVQ VNPNNGDFLP 1500
LLTASSQGPQ TLFSPFNQWP DYVLPLAITV PIVVIVLSVT LGLAIGIPMH KNKQALKAGF 1560
ALSNQKVDVL TKAVGSVFKE IINRTGISQA PKRLKQTSAA KPGAPRPPVP PKPGAPKPPV 1620
QPPKKPA 1627
<212> Type : PRT
<211> Length : 1627
SequenceName : SEQ ID 124
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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KAALAEDNGT ETILRVNFGE ALKSWYQNNK DRNIATRLTI FSENVEDEHD NLLDQKQQAE 120
PINWPIELQK EYDQWGGSES SWKALKLYDR LIADFQSLIF SNIVANVQLT DGSDQFKPTT 180
KDNLDSTSNK IKFVNSKPND PNGEFFANLQ AYLFAQWVVE ENPLPLTQAF FAYQAPKDGL 240
DSLYDQAAIG SALQLGYAFP AFREPNNGQS QGKTTFDPTP NSAQNFGDFI KAVFPEQKNG 300
QTQQSNTSSR TGLFDWQTKW NTNGAANKLL VTKSNLRGAF KGVGLATAII DQYEYLVGGS 360
KTSSLPEVKV DSNKSNQNPL DSFFMEGKDA VAIRSIVSRA KIAMTDQTPG FKVNPAFVKV 420
KQSQQNDTFY QNQRKLSGGQ SGDNNSQGKH HYLQDAVRLT SSQAMAAAST GADSSSGTNV 480
GGSSGGNSVL IPLPRSAALT HTQQQVQQTT STLQTPVYAR GDDGTYALAI DGGDYFLANN 540
KRDFTKQADI LLYRYLQAKS NNFKENGVEF SLNLLESGSL FQTWAQTGLT AKLYGALVAM 600
MGSGQGTQVK GSVQGSSRAA SVSVQTTQQN RQQSTDTQES EVVKLAKSLL KSSADLAKPF 660
TDNPTFKKAL TDIQSEYKDY LAAAGKLSEF KKDLGEVSGL QQAIIDRADK YIQLEKQAQK 720
SAIGLGQPLP YQRASDGSYP ALEKFFIPED SAADGKVKAS ESGSAALVTL KTTDSQKSTN 780
TVKQPDIKPT RENNDKKLKQ LTSDVETKAS SLITKWGATP QIGSQFSEIV SLKSKDNKPQ 840
TNMILALLSD VGIKWTKILN SFKEWFFTNT NDFKNNYDSE KKELKGNEYK DFNDLVKQTL 900
YLRSWQRLTS KEKFGYYKEL GSVKAQAAQS GMVSLSSSAA VANAVASSGM QKSGDQTLLE 960
LGKKAFESEL EASSSDGQYK YLRFLSTLMW LVKDGAKNYK RLLQQAITVG TRAFVSWTVS 1020
YDDTATASAA AAKAQVAVLK TAQATNTQSD NPFNKFVQNP DYVQGSETNW FNDKSTPIKP 1080
DSLLESESTY NFTAEPFDDK TKSQKRSTGG TTNEKHFFGF NGLTINSPQS VSTASAGLTE 1140
QIFNNFGQLV TSSDKSGALS QYKDKATLKR LIQNTNSDAE LNAFGEVLHR AVNVDTSNLG 1200
RFNSSGEPLI SFDNKKKFLV DVVDKLDDVY FNKFEGYVGQ TKVKMSDSSS SSQGTKTIRK 1260
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<212> Type : PRT
<211> Length : 1300
SequenceName : SEQ ID 125
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MKKLLIKPQF WFLTLGGFIS SSVILVACAT PSNSALQTVF KARSNQFFNG EQGSLQNALA 60
TALKDPEANK QFVAAPLLKA LTAWYENNQD KQVTQFFKDT KKSVDEQYNQ AVDKVVSASR 120
NKNLFVQQDL LDSAGGVRNL KSPEVVWTAH 150
<212> Type : PRT
<211> Length : 150
SequenceName : SEQ ID 126
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MQQQGETKDQ YNTFGLRLVR NSVGVSVLGL DGFVKFIKGG SGGSNGGSSS AKKIDKEEQK 60
KFLKFRAFQA KIGTFYNTNF AFSFPLNETL KGWFDKHRGL ILANALVKVT LDTKEKASKA 120
LVDAFSSYKN WLSEYTPVGL ATTMISFYFD QMKALNNKLL ERVRSLNQNV NQANPTPWLN 180
GLSAKLPYVN TNGNYEKLNN YFTFLITKVL WPKVGTEDTN VSEEKSKLKT KTEDVNKIRE 240
KILNNIDSKL KTFVQKLKPT LAPRPAYSNV ILLNINNDKV WSAGANWSLA VLLDPKKVNP 300
LSFMLLKQMF DQNSLFKKAK TLFENIQNKA KTSGSGKSGT TTNDDADALS KVIGNYYYNT 360
WAKLTDKSIY GNLKDDKFDD LFKLAFDSSI NEKSFNVDYK AVIEHYRFIY TLEWLVDKNL 420
KNFKDLLKAN LKFGEIAFIA YKNTETQNFS NPQGIFGSYF NYENETNAAK SATQIIDPNS 480
FFYKTTTKPE AKTTQSANTA VMVQNTQMNN QQTNSYGFTG LSTSSGSMLG AATQQAILDQ 540
ITKTSLQQYG SQADLKKIIG ETKNQLLLDR IANQLIALKP NTSGNSGTQK TIAAYFQTDA 600
VGNPTLDFKA KQKLLLDVLD QYKDFFGNNA QAVQRDSGKS GTGNYLTYTD GSDKITYLQF 660
SYKDIDGLSL SSSNGTSSKF ASDVVAALLL FQAAYKGTQQ LALSSINKPQ LPIGDKRIKT 720
GIDLLK 726
<212> Type : PRT
<211> Length : 726
SequenceName : SEQ ID 127
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :

MKSFLRKPKF WLLLLGGLST SSIILSACAT PSNSALQAVF KPTSNQFFNG EHGTIQSALN 60
TALRDPETNK KFVAAPLLKA LEAWYENNQD KNITQFLKDT KTNVDNQYKT VVDKVVSAPR 120
NKSLFVQQDL LDSSGGSEAT WKARKLFEQL ISDFASRVFQ KNYLSYKENG KVSAGPFLYD 180
TISKNSNWQN IVFDAVNFPE TNDDFFAKIQ SEVFDQWAEY TDPTIISSVT LKYSAPN 237

<212> Type : PRT
<211> Length : 237
SequenceName : SEQ ID 128
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MINFLFNQMN ALNNKFLERA KALNQNVNQA NPTPWLNGLS AKLPYVRTNG NYEKLNNYFT 60
FLIVKYMWKK VGNEDASLSK DSSINKLKTK TEDVNKIRDK ILEDIQKKVQ EFVKNKLKPT 120
LAPRQTYSNV ILLNVNNDKV WSMGANWALA NLLDTSKINP LSFMLLKQTF DQNDLFKKAK 180
KLFEDIQSKT NGGSSGGMQG SNTSSSEGAD ALSKVIGNYY YNSWAKLTDK SIYGNPKDNK 240
FDDLFKLAFE DSINEKSFNV DYKAVIEHYR FIYTLEWLVN GNLKNFKDLL KANLKFGEIA 300
FIAYKNTETK EFSNPQGVFG SAFNYENETN EVKIAAQNLD PNNFFYKTTT KPEEVKTAQN 360
GASMMVMQQK MQSTMQDSNH YGFTGLNTST SSMLGAATQQ AILDQITKNS LQQYGSQQEL 420
KTLIEKTNNQ LLLDRIASQL SGLNPSTTGN SNNGKGKNIA TYFQLDAIGN PTLSFQQKRK 480
LLLDVLDQYK DFFGTNTQAA QRDSGKGGHG SYSTYQDGSD KITYLQFSYK DIDNLSLSDK 540
GNSKLASDVV AALLLFQAAD KGTQQLALSA IN 572
<212> Type : PRT
<211> Length : 572
SequenceName : SEQ ID 129
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
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TALKNPVANK QFIAAPLLKA LEAWYENNED KKITQFLKDT KSNVDSQYTT AVDKVVSASR 120
NKSLFVQQDL LDNAGGSEAT WKAQKLLEQL ISDFASRVFQ KNYLNYKKDG QVSTGPFTYD 180
ELHKEESWKN FEFSAPRFSE TNDDFFAKIQ SQVFDQWVEY TDPTLISQVN YKYSAPSQGL 240
GQIYNREKLK DKLTPSYAFP FFAEEKDIAP NQNVGNKRWK QLVKGEGAIT DNNIGQSGTN 300
SQKTGLLKYR NESNKGDFLD FPLNLSDTNE TKQLVDASNI VDQLEAANLG AALNLKLQVF 360
EQDNDELPQI KELKEDLNNT IVVDKSKDVE KASKTNALFY NDQEGKQQQS DSDPIAGALD 420
DIFAQNTSEG TNLSKLAEQV KKAAATKMEA KTAVLRTNNS KGQQNNYVVL DAAIPTFNST 480
TSKSKNNSAS NEVLVALKSG SINLRQVQQT DQNSYSPIKF RIVRNSTGVT VFGLDGGSYY 540
LKQDSTNKKS VSKQSLTLLT KSSSGNSNKV LRDLDKQKQF LKFRAFQAKT NTFYSTNFAF 600
SFPLNETLKS WFDKHRELIL ANALVNASLD QKDKASKALT EAFNPYKELI KEFAPVALAT 660
TMISFYFDQM KALNNKLLER ARNLNQNVNQ ANPTPWLNGL SAKLPYVNTN GNYEKLNNYF 720
TFLITKTLWP KVGQEETSIS EESNKLKTKT ADVDKIRDKI LENIQTKVND FVKNKLKPAL 780
APRPAYSNVI LLNVNNDKVL SSGANWSLAS LLQSDKVNPL SFMLLKQAFD NNDLFKKAQK 840
LFKDIQEKSS NNGGMQSSST TNSDADALSK VIGNYYYTTW AKLTDKSIYG NPKDNKFDEL 900
FKLAFEASID EKSFNVDYKA VIDHYRFIYT LQWLVDQKLK NFKSLLKTNL KFGEVAFIAY 960
KNTETTNFSN PQGVFGSYFN YENSASEVKE STQTLDPNNF FYKTTTKPTV QAIQQVASLA 1020
LVQKQQMQQN STDHYGFTGL STSTSSMFDA SSRDAILQQI TKTSLQQYGS KDQLKKIIQG 1080
TNNQLLLDRI AVQLSGLNPS TTNGGSGKTI ATYFQVDAVG NPTLDFQAKR KLLLDLLDQY 1140
QNYFGNGAQK SQRDSTPSGT GNYLTYQNGS DKYTYTQFTY QDIDSLSLTT TSGTNNKIAS 1200
DVVAALLLFQ AADKGTQQLA LSAINKPQLN IGDKRIESGL KLLK 1244
<212> Type : PRT
<211> Length : 1244
SequenceName : SEQ ID 130
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MVGSGAAGSA SSLQGNGSNS SGLKSLLRSA PVSVPPSSTS NQTLSLSNPA PVGPQAVVSQ 60
PAGGATAAVS VNRTASDTAT FSKYLNTAQA LHQMGVIVPG LEKWGGNNGT GVVASRRDAT 120
STNLPHAAGA SQTGLGTGSP REPALTATSQ RAVTVVAGPL RAGNSSETDA LPNVITQLYH 180
TSTAQLAYLN GQIVVMSSAR VPSLWYWVVG EDQESGKATW WAKTELNWGT DKQKQFVENQ 240

LGFKDDSNSD SKNSNLKTQG LTQPAYLIAG LDVVADHLVF AAFKAGAVGY DMTTDSNAST 300
YNQALVWSTT AGLDSDGGTR LW 322
<212> Type : PRT
<211> Length : 322
SequenceName : SEQ ID 131
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MPVFLKLTHT IRKVLRVARL SRLALLSLTA VIFSGCANIN LISAVGSSSV QPLLSKLSSH 60
YVLNHNDKDN LVEISVQAGG SSAGVKAITK GLADIGNVSK NTKSYAEENK QLWMDKKLKT 120
ITLGKDAIAV IYKAPSEFKG KLVLTKDNLN DLYDLFAGSK SVDINKFVEN GQTTKNSNHN 180
LIGFPRTGGA FASGTAEAFL KFSGLTQTKT LDKDSKEILE GQRNYGPNAR PTSETNIEAF 240
NTFVTTLRQP NLYGMVYLSL GFVNNNMNLI KSEGFEVLKV KYDNNAVTPS SQAVSSNTYK 300
WVRPLNSVVS LLPKQKTLPS IQRFFNWLLF SNNSEIKKIY DDFGVLELTA DEKKKMFKTG 360
NAEMSNIANF WVDDYSLNNQ TFGAL 385
<212> Type : PRT
<211> Length : 385
SequenceName : SEQ ID 132
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSFAVLPPEI NSARLYVGAG LAPMLDAAAA WDGLADELGS AAASFSAVTA GLAGSSWLGA 60
ASTAMTGAAA PYLGWLSAAA AQAQQAATQT RLAAAAFEAA LAATVHPAII SANRALFVSL 120
VVSNLLGQNA PAIAATEAAY EQMWAQDVAA MFGYHAGASA AVSALTPFGQ ALPTVAGGGA 180
LVSAAAAQVT TRVFRNLGLA NVGEGNVGNG NVGNFNLGSA NIGNGNIGSG NIGSSNIGFG 240
NVGPGLTAAL NNIGFGNTGS NNIGFGNTGS NNIGFGNTGD GNRGIGLTGS GLLGFGGLNS 300
GTGNIGLFNS GTGNVGIGNS GTGNWGIGNS GNSYNTGFGN SGDANTGFFN SGIANTGVGN 360
AGNYNTGSYN PGNSNTGGFN MGQYNTGYLN SGNYNTGLAN SGNVNTGAFI TGNFNNGFLW 420
RGDHQGLIFG SPGFFNSTSA PSSGFFNSGA GSASGFLNSG ANNSGFFNSS SGAIGNSGLA 480
NAGVLVSGVI NSGNTVSGLF NMSLVAITTP ALISGFFNTG SNMSGFFGGP PVFNLGLANR 540
GVVNILGNAN IGNYNILGSG NVGDFNILGS GNLGSQNILG SGNVGSFNIG SGNIGVFNVG 600
SGSLGNYNIG SGNLGIYNIG FGNVGDYNVG FGNAGDFNQG FANTGNNNIG FANTGNNNIG 660
IGLSGDNQQG FNIASGWNSG TGNSGLFNSG TNNVGIFNAG TGNVGIANSG TGNWGIGNPG 720
TDNTGILNAG SYNTGILNAG DFNTGFYNTG SYNTGGFNVG NTNTGNFNVG DTNTGSYNPG 780
DTNTGFFNPG NVNTGAFDTG DFNNGFLVAG DNQGQIAIDL SVTTPFIPIN EQMVIDVHNV 840
MTFGGNMITV TEASTVFPQT FYLSGLFFFG PVNLSASTLT VPTITLTIGG PTVTVPISIV 900
GALESRTITF LKIDPAPGIG NSTTNPSSGF FNSGTGGTSG FQNVGGGSSG VWNSGLSSAI 960
GNSGFQNLGS LQSGWANLGN SVSGFFNTST VNLSTPANVS GLNNIGTNLS GVFRGPTGTI 1020
FNAGLANLGQ LNIGSANLGD FNLGSGNVGS FNVFSGNQGS YNIGPANLGN YNIGFANLGN 1080
YNIGFGNAGD FNQGFANTGN NNIGFANTGN NNIGIGLSGD NQQGFNFAGG WNSGTANIGL 1140
FNSGTNNVGI GNSGTGNWGI GNSGSGNTGI GNTGSTNTGF FNTGIVNTGV ANAGSYNTGW 1200
YNTGDTNTGI ANLGDFNTGF YNTGNFSTGF ANQGDIATGA FITGDMGNGA FWRGDQQGLF 1260
SAGYRVHVPE IPAHVTVEVP VNIPITASFT NTVYSGITLE QINFGFTIDI AGIPLLAGAI 1320
SKAVLPPITG TGPAITVNIG DPGGSTAIRI PATASVGPFD VTFVNIAATT GFFNATTDPS 1380
SGFFNGGPGT VSGIANIGAN ISGFQNVANS ATSGFNNYGS LQSGLANLGD TVSGVFNTGI 1440
GAPANVSGMF NIGSNLAGFF HDQATGMSMF NLGLGNIGQF NVGFSNVGDS NAGLANIGSF 1500
NLGSGNLGSF NVFGGNQGSY NIGPANLGNY NIGLGNLGSY NFGFGNAGDF NLGFANTGNN 1560
NIGFANTGNN NIGIGLSGDN QQGFNFAGGW NSGSGNSGLF NSGTNNIGLF NSGTGNIGIG 1620
NSGTGNWGIA NTGDTNTGIF NTGDVNTGLL NAGNVNTGIF NTGHYNTGSF NAGSFNTAGF 1680
NPGSYNTGYL NTGSYNTGLA NSGDVNTGGF ITGNYSNGFW WRGDYQGLAG ISQTITVPDT 1740
AVPVKLHVPI FLDIPVTGTL GTFTVHGFRF PEITGDIFLI GIPFNAATLD AFSFPNISIV 1800
LPNIGINLGS GPDPLIDIAG TGGLLPIKIP LIDIPAAPGF GNSTTTPSSG FFNAGTGTVS 1860
GVGNVGSNSS GFFNLTSGSS GISGVQNFGE LISGGFNFGN TVSGLVNAST LGLSMPANLS 1920
GGGNVGATVA GFVNNTQILN LGFGNVGSGN VGHGNIGDSN VGLGNLGNAN VGHGNIGSFN 1980
VFSGNRGSYN IGPANLGNYN IGLGNLGSYN FGFGNAGDFN LGFANSGSNN IGFANTGNNN 2040
IGIGLSGHNQ QGFGSWNSGT ANTGLFNSGT NNIGLFNSGT GNIGIGNSGI GNTGIGNPGV 2100
GNTGLGNSGT GNWGLWNPGT GNMGVANVGT YNTGGYNVGS TNTGIANVGI ANTGSYNTGS 2160
TNTGSFNDGD FNTGFYNTGD YNTGFYNTGD VNTGAFIGGN FSNGAFWQSD HQGQWGAHYA 2220
ITVPQIPLLN FSLNIPVNIP IHLDFGTLAV NGFQIPAITL RALGVTHFSV GPIIVPRIAG 2280
TLPVIDINIG DPGGSSSIPI TITSGAGPVV IPLLDIPPAP GFGNSTTGPS SGFFNSGTGS 2340
SSGFGNVGAN NSGFWNTAFA GIGNSGLQNF GSLQSGWANL GNTVSGFYNT SAADFATPAN 2400

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LSGLSNVGAD LTGVLRGPNG STFNAGLANL GQFNVGSANL GSANLGSANL GSANLGNSNV    2460
GFGNIGNANI GGANIGDFNV GIANTGPGLT AAVNNIGIGN TGNYNIGVGN TGNYNIGFGN    2520
TGNNNIGIGL SGDNQIGFGP LNAGIANMGL FNLGDNNFGM ANAGNFNQGI ANTGNNNIGL    2580
FNTGNNNVGI WLTGDGLSGF SSLNSGAGNT GFFNSGTANT GLFNSGTGNT GLFNSGTGNV    2640
GIGNMGTGGF GVGLSGDSQV GIGGTNSGSF NIGLFNSGTG NVGIGNSGTG NVGIGNTGTG    2700
NTGIGNSGNY NTGLLNAGLV NTGIANPGNH NTGLFNIGTF NTGIANPGHY NTGSYNTGSY    2760
NTGMANAGDY GTGAFITGSM NNGLLWRADR QGLLAANYTI TIERPAAFLN VDIPVNIPIT    2820
GDITNVSIPA ITFPRIDASG SVDIGILSGT VLAPVGPITL HGGDASAPLD TPIEIDFGPS    2880
PAINLNIGKP DGSTVINIVG GAGAGPISIP IIDLRPAPGF FNATTGPSSG FLNWGAGSAS    2940
GLLNFGNNSG LYNFATSSMG NSGFQNYGSL QSGWANLGNS ISGIYNTGLG APANVSGLLN    3000
IGTNLAGWLQ NGPTETTFSV GLANLGFWNL GSANIGNYNL GSANIGVYNL GSANIGDFNL    3060
GSANIGDFNL GSANIGSSNI GFGNVGPGLT AAIGNIGFGN TGNGNIGIGN TGTGNIGFGN    3120
TGNGNIGIGL TGDTMTGFGG WNSGTGNIGL FNSGTGNIGF GNSGTGNWGI GNSGDYNTGI    3180
GNTGSTNSGF FNTGLVNTGI GNSGDYNTGL FNAGNTNTGS FNPGDYNTGG FNPGNYNTGY    3240
FNPGNSNTGI ANSGDVNTGA FNSGNYSNGF FWRGDYQGLG GFAYQSAVSE IPWSYDRFQH    3300

<212> Type : PRT
<211> Length : 3300
      SequenceName : SEQ ID 133
      SequenceDescription :

Sequence
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<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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LRDGAGTAAI NLGLANHGNL NVGFASLGGF NFGGATIGHN NVGIGNTGIF DVGLANLGSY     120
NIGFGNLGDD NLGFGNFGSY NIGFGNVGND NLGFANAGGG NIGFANTGSN NVGFGNTGSN     180
NVGIGLTGNG QIGFGSFNSG SGNIGLFNSG SNNIGFFNSG SGNFGIANSG SFNTGIGNTG     240
NTNTGLFNSG DVNTGAFNPG SFNTGSFNTG SFNTGGFNPG NTNTGYLNIG NYNTGIANTG     300
DVDTGAFITG NYSNGLFLSG DYQGLVGLNL VIDMPLPISL GVNIPIDIPI TASAGNITLM     360
GVTIPPTGDI VLSSIAGQRA HFGPITIPNI TVVGPTTTVA IGGPNTAITI TGGGAIRIPL     420
ISIPAAPGFG NSTTNPSSGF FNTGAGGASG FGNFGGANSG FWNLASATSG ASGLLNVGAL     480
GSGLANVGTT VSGFYNTSTS DLATPAFNSG LANISTSIAG LLRDSTGTMV LNLGLANHGT     540
LNVGIANLGD YNIGFANLGS ANFGSANIGG NNIGGANTGI FDIGLANLGS YNIGFGNFGD     600
DNLGFGNLGS YNVGFGNLGN DNLGFANTGS NNIGFANTGS NNIGIGLTGD GQIGFGSLNS     660
GSGNIGLFNS GSGNIGFFNS GNGNVGIGNT GTANFGLGNT GSTNTGFFNS GDVNTGIGNT     720
GSFNTGSFNP GDSNTGDFNP GSYNTGLGNT GDVDTGAFIS GSYSNGFLWS GNYQGLIGLH     780
AALAIPEIAL TFGVDIPIHI PINIDAGVVT LQGFSIVAAE NNIDFTPIII PTINITLPTA     840
AITVGGPTTS IGITASAGIG SITIPIIDIP ATSGFGNSTT SPSSGFFNSG AGSASGFLNV     900
VAGASGISGY LNVGALGSGV TNVGHTVSGF YNASALDLVT PAFASGLMRD GMGTMTLNLG     960
LANLGSNNAG FGNTGIFDVG VANLGNYNIG FGNFGDDNLG FANLGSYNIG VANTGSNNIG    1020
FANTGSNNIG IGLTGTGQIG IGALNSGSGN IGLFNSGDGN IGFFNSGTGN FGIGNTGTGN    1080
FGIGNSGSTS TGLFNSGDGN TGGFNPGNFN TGNFNTGSFN TGGFNAGNTN TGHFNTGNYN    1140
TGIANTGDVS TGAFISGNYS NGILWRGDYQ GLIGYSYALT IPEIPAHLDV NIPIDIPITG    1200
SFTDLVVDNF TIPIIGFESF AFSFHIHTEP DIGPIIVPSF VLSVPTFAIA VGGPTTAINI    1260
SATAGLGPIT IPIIDIPAAP GIGNSTTSPS SGFFNTGAGT ASGFGNVGGN TSGLWNLASA    1320
ASGVSGLLNV GALGSGVANV GNTISGIYNT SPLDLGTPAF GSGLANIAGL LQGGAGTTIL    1380
DLAGLGNLNV GLANLGGSNF GIGNTGIFNV GFANVGNHNI GLANLGNYSV GFANSGNYHI    1440
GIANTGSANI GFANTGSGNI GIGLTGTGQI GFGSFNSGSH NIGLFNSGDG NVGFFNSGTG    1500
NVGIGNTGTA NFGIANSGSF NTGLGNTGST NTGLFNPGNV NTGVGNTGSI NTGSINTGSF    1560
NTGSTNTGSF NLGDHNTGSF NSGDYNTGYF NAGDYNTGVA NTGNVNTGAF ISGNYSNGFF    1620
WRGDYQGLIG LSTTITIPEI PYRYDLSVPI DIPITGTVVA TTPNSFTIPG FQIRVLLGPA    1680
AVLVNEMIGP ITIDVNQVIA IDSPIQQTIS MVGTGGFGPI PIGISIGGTP GFGNSTTGPS    1740
SGFFHTGAGH VSGFGNFGAG NMSGSGNFGA GNSGFFNAGG LGNSGLLNFG ALQSGLANLG    1800
NTISGVYNTS TLDLATPAFG SGIANIGANL AGLFLDNTGN LTLNFGVANQ GGLNAGIGNL    1860
GSVNIGFVNT GDSNLGIGNL GDLNFGGVNI GGNNIGIANT GIFDIGLANL GSYNIGLANL    1920
GDDNLGFGNA GSYNIGFANF GSDNLGFANT GSYNIGFANT GNNNIGVGLT GNGQIGIGSL    1980
NSGSNNIGLF NSGSGNIGFF NSGTGNVGIF NTGTGNFGLA NSGGFNTGIG NAGSTNTGVF    2040
NPGDLNTGSF NPGSFNTGGF NPGSGNTGYL NTGDYNTGVA NTGDVDTGAF ITGSYSNGFL    2100
VSGDYQGLIG LPLLGIPVTP GYFNLTGGPS SGFFNSGAGS VSGFVNSGAG LSGYLNTGAL    2160
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<212> Type : PRT
<211> Length : 2204
      SequenceName : SEQ ID 134
      SequenceDescription :
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Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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EYQAISAQVA AYHQRFVQAL STGAGAYASA EAAAAEQIVL GVINAPTQAL LGRPLIGDGA 120
NATTPGGAGG AGGLLFGNGG AGAAGAPGQA GGPGGPAGLW GNGGPGGAGG SGGGTGGAGG 180
AGGWLFGVGG AGGVGGAGGG TGGAGGPGGL IWGGGGAGGV GGAGGGTGGA GGRAELLFGA 240
GGAGGAGTDG GPGATGGTGG HGGVGGDGGW LAPGGAGGAG GQGGAGGAGS DGGALGGTGG 300
TGGTGGAGGA GGRGALLLGA GGQGGLGGAG GQGGTGGAGG DGVLGGVGGT GGKGGVGGVA 360
GLGGAGGAAG QLFSAGGAAG AVGVGGTGGQ GGAGGAGAAG ADAPASTGLT GGTGFAGGAG 420
GVGGQGGNAI AGGINGSGGA GGTGGQGGAG GMGGSGADNA SGIGADGGAG GTGGNAGAGG 480
AGGAAGTGGT GGVVGGAAGKA GIGGTGGQGG AGGAGSAGTD ATATGATGGT GFSGGAGGAG 540
GAGGNTGVGG TNGSGGQGGT GGAGGAGGAG GVGADNPTGI GGTGGTGGKG GAGGAGGQGG 600
SSGAGGTNGS GGAGGTGGQG GAGGAGGAGA DNPTGIGGAG GTGGTGGAAG AGGAGGAIGT 660
GGTGGAVGSV GNAGIGGTGG TGGVGGAGGA GAAAAAGSSA TGGAGFAGGA GGEGGAGGNS 720
GVGGTNGSGG AGGAGGKGGT GGAGGSGADN PTGAGFAGGA GGTGGAAGAG GAGGATGTGG 780
TGGVVGATGS AGIGGAGGRG GDGGDGASGL GLGLSGFDGG QGGQGGAGGS AGAGGINGAG 840
GAGGNGGDGG DGATGAAGLG DNGGVGGDGG AGGAAGNGGN AGVGLTAKAG DGGAAGNGGN 900
GGAGGAGGAG DNNFNGGQGG AGGQGGQGGL GGASTTSINA NGGAGGNGGT GGKGGAGGAG 960
TLGVGGSGGT GGDGGDAGSG GGGGFGGAAG KAGGGGNGGR GGDGGDGASG LGLGLSGFDG 1020
GQGGQGGAGG SAGAGGINGA GGAGGNGGDG GDGATGAAGL GDNGGVGGDG GAGGAAGNGG 1080
NAGVGLTAKA GDGGAAGNGG NGGAGGAGGA GDNNFNGGQG GAGGQGGQGG LGGASTTSIN 1140
ANGGAGGNGG TGGKGGAGGA GTLGVGGSGG TGGDGGDAGS GGGGGFGGAA GKAGGGGNGG 1200
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GSGGTGGTGG DAGVGGLANT GGTAGNAGIG GAGGRGGDGG AGDSGALSQD GNGFAGGQGG 1440
QGGVGGNAGA GGINGAGGTG GTGGAGGDGQ NGTTGVASEG GAGGQGGDGG QGGIGGAGGN 1500
AGFGAGVPGD GGIGGTGGAG GAGGAGADGD PSIDGGQGGA GGHGGQGGKG GLNSTGLASA 1560
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GGDGGAGDSG ALSQDGNGFA GGQGGQGGVG GNAGAGGING AGGTGGTGGA GGDGQNGTTG 1680
VASEGGAGGQ GGDGGQGGIG GAGGNAGFGA GVPGDGGIGG TGGAGGAGGA GADGDPSIDG 1740
GQGGAGGHGG QGGKGGLNST GLASAASGDG GNGGAGGAGG NGGAGGLGGG GGTGGTNGNG 1800
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<212> Type : PRT
<211> Length : 1901
SequenceName : SEQ ID 135
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
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AGGAGGSGGW LLGNGGVGGA GGQSLLGGAT GGAGGNAGLF GVGGTGGPGG PGGPGGVGGT 240
GGAGGLGGTL YGAGGHGGAG GPGPIGGVGG HGGVGGAAGL LGVGGHGGAG GHGAEGVAGA 300
AGEDLSPHGT SGGVGGDAGD GGTGGRGGWL AGAGGAGGAG GVGGTGGAGG AGFSRALIVA 360
GDNGGDPGAG GAGGTGGAGS TIGAHGAAGA SPTSGGNGGA GGNGAHFSSG GKAGGNGGAG 420
GAGGLVGNGG AGGAGGNGAP GAPPSGGDPN GGGGGAGGAG GKGGDGGAQA GDGGAGGAGG 480
KGGNGGNGAT GATGLNGLGA GADGTDGGKG GNGGAGGGGG AGGQGGKALA ATHQDGSMGA 540
GGAGGNGGAG GMGGDGGNGA KGTFDNGGDG VGGNGGNGGS RGIGGAGGIG GAGSTAGADG 600
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PTTAGESGTS GQNGGAGGAG GAGGRGGDFG GDGGTGGAGG NGANGANATT PGAKGGDGGH 720
GGPGAQGGNG GQGGPGGLAG NLFGQNGIQG VGGSGGKGGA GGLAGDGGNG ANGNFAFGDG 780
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GPAGSILHDG GNGGHGGHGA ASGGNGGPGG HGGNGGNGGT GANGGNGGIG GTGGAGSTGA 1080
KGVLGTNEGD GGDGGRGGNG GRGGNGGQGL TGAGGNGGTG GTPGNGGNGG NGASGDLVTS 1140
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<212> Type : PRT
<211> Length : 1329
SequenceName : SEQ ID 136
SequenceDescription :

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<213> OrganismName : Mycobacterium tuberculosis H37Rv
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GTGGWLAGGG GVGGMGGAGG GAGGAGGNAG LFGNGGAGGA GGAGGGAGGA GGNAGWFGHG 240
GAGGVGGVGA AGANGATPGQ DGAAGVAGSD DGAGGDGLAG SDGGDGGAGG VGGNGGRGGW 300
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GGAGGAGGSA GLLGYVGRAG DGGAGGGGGL GGAPGDGGAG GNGGSWLAAG DGGAGGHGGD 420
PGLGGAGGAG GASGGAGARA GANGLAAGND GPVSGGNGGK GGNGAHAPVA GGHGGNGGAG 480
GNGGLVGDGG AGGHGGDGAA GAGYADMTAI FLGSSGTPGE DGGNGGAGGA GGAGGAHAGD 540
GGAGGAGGNG GAGGAGGNGA HGFNAVLVSD GGNGGDGGAG GRGGDGGAGG AGGDAPAGRA 600
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NGANVGEDGA DGTLSGQPGE GSEANGGQGG VGGGGAGGAG GDGGAGSSAL GSGGNGGRGD 780
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GGWGRPGGQG GFGSTSGAHG KAGFGAPGGD GGDGGNGGHG GDGNGSFADA GDGGPGGNGG 1560
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<212> Type : PRT
<211> Length : 1660
SequenceName : SEQ ID 137
SequenceDescription :

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<213> OrganismName : Mycobacterium tuberculosis H37Rv
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GGNGGWLFGA GGTGGIGGTG APGAMGGTGG NGGNGALLIG GGLGGAGGM GGTGGGTGGT 240
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GDGAAGDAAA SAGGTGGKGG QGGDGGTGGA GGAGPVLFGH GGAGGMGGQG GTGGMGGAGG 360
DGTTVIAAGT GGEGGTGGAA GAGGAAGARG ALTSGGLAGG VGAGGTGGTG GTGGNGADAA 420
AVVGFGANGD PGFAGGKGGN GGIGGAAVTG GVAGDGGTGG KGGTGGAGGA GNDAGSTGNP 480
GGKGGDGGIG GAGGAGGAAG TGNGGHAGNT GDGGDGGTGG NGGNGTGGVN GADNTLNPDT 540
PGGAGEPGGA GGAGGAGGAA GGPGGTGGTG GNGGNGGNGG NGGNGGNGGN GGNAGNNSTN 600
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DGEAGFSGGA GGNGGVGGAA GANGGTGGSG GNGGDGGAGG IGGAGGNGIP GTGTEPAGGT 720
GAKGGDGGDG GAGGAGGNAG GAGGQGGNAG QGGAGGAGGN AVIPGDGVGK APHGDAGGSG 780
GDGGKGGQGG SGGTGGSGAP IGGGAGGTGG SGGHAGKGGA GGIGAQGTTI TVPGNGGNAG 840
DGGNGGNAGA GGNGGSGDFG GNTTSGASGS GGNGGNAGTA GSGGAGGTGG TGLSGGNGGN 900
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SPMVAPPPPT PITQVQQGGD GGAGGTGSTN ANDGTATGGK GGEGGVGSIL GGPGGNGGTG 1080
GNASATGTNG VANAGNGGKG GDGGQFGAGG NGGAGGSVTD GSAGSTAGNG GNGGNATNGT 1140
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GGANGGDGGA GGAGGAGGRG GKGIDGGFGG DGGNGGSNNG TGAGGNGGNG GTGGVGSVGA 1260
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<212> Type : PRT
<211> Length : 1381
SequenceName : SEQ ID 138
SequenceDescription :

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<213> OrganismName : Mycobacterium tuberculosis H37Rv
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GSGTAGGAGG IGGNGGAGGA GGVLMGNGGN GGAGGEGGPG GAGGAGASGA HATNLGADGQ 300
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NLGAGGTGGN GGNPGAGGAG GAGGASVGGS AHGANGAPGT TSTSGGNGGD GGKGADAISS 420
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ASGQNGSQGA GGDGGAGGNG GTPGNGGHGA AGALGVNGGV GGAGGHGGDP GVGGAGGQGG 600
SGSTPGANGA PGNTPTSGGN GGNGGRGADA TGFGQTGASG GRGGDGGLVG NGGAGGAGGN 660
GSKGLPGLGR LGNPGLDGGT GGNGGAGGSG GAWAGNGGTG GAGGTGGVGG TGGSGSDGVN 720
GSSAGADGHP GGTGGVGGTG GKGGDGGDGG AAPNGVAGSQ GPGGAGGDGG TGGVGGNGGR 780
GIDGADGATA GARGQDGGAG GAGGKGGRGG TGGPGGAGPA GTTGSQGAGG NGGSGGTGGD 840
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GSQGAGGDGG AGGAGGTGGT GGDGGRGAHG TLFSSLAGTG GTGGNGGTGG TGGTGGAGGA 1140
GGTGSTLGAT GATGAAGRAG NGGVGGSGGL GSAFGPGGTG GMGGAGGTST VSAGGDGGRG 1200
GFGGDGLDAS SGGNGGDGGH GGDGFRTAGA GGRGGDGGKG ADPGGLFPIP GAGGKGGTGG 1260
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<212> Type : PRT
<211> Length : 1306
SequenceName : SEQ ID 139
SequenceDescription :

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<213> OrganismName : Mycobacterium tuberculosis H37Rv
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WAIDVSVMSA YHAGASAVAS ALTPFTAPPQ NLTDLPAQLA AAPAAVVTAA ITSSKGVLAN 180
LSLGLANSGF GQMGAANLGI LNLGSLNPGG NNFGLGNVGS NNVGLGNTGN GNIGFGNTGN 240
GNIGFGLTGD NQQGFGGWNS GTGNIGLFNS GTGNIGIGNT GTGNFGIGNS GTSYNTGIGN 300
TGQANTGFFN AGIANTGIGN TGNYNTGSFN LGSFNTGDFN TGSSNTGFFN PGNLNTGVGN 360
TGNVNTGGFN SGNYSNGFFW RGDYQGLIGF SGTLTIPAAG LDLNGLGSVG PITIPSITIP 420
EIGLGINSSG ALVGPINVPP ITVPAIGLGI NSTGALVGPI NIPPITLNSI GLELSAFQVI 480
NVGSISIPAS PLAIGLFGVN PTVGSIGPGS ISIQLGTPEI PAIPPFFPGF PPDYVTVSGQ 540
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YSLPAIPLGI DVGGGLGPFT VFPDGYSLPA IPLGIDVGGA IGPLTTPPIT IPSIPLGIDV 660
SGSLGPINIP IEIAGTPGFG NSTTTPSSGF FNSGTGGTSG FGNVGSGGSG FWNIAGNLGN 720
SGFLNVGPLT SGILNFGNTV SGLYNTSTLG LATSAFHSGV GNTDSQLAGF MRNAAGGTLF 780
NFGFANDGTL NLGNANLGDY NVGSGNVGSY NFGSGNIGNG SFGFGNIGSN NFGFGNVGSN 840
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GILWRGDYQG LIGYSDTLSI PAIPLSVEVN GGIGPIVVPD ITIPGIPLSL NALGGVGPIV 1080
VPDITIPGIP LSLNALGGVG PIVVPDITIP GIPLSLNALG GVGPIVVPDI TIPGIPLSLN 1140
ALGGVGPIVV PDITIPGIPL SLNALGGVGP ITVPGVPISR IPLTINIRIP VNITLNELPF 1200
NVAGIFTGYI GPIPLSTFVL GVTLAGGTLE SGIQGFSVNP FGLNIPLSGA TNAVTIPGFA 1260
INPFGLNVPL SGGTSPVTIP GFAINPFGLN VPLSGGTSPV TIPGFTIPGS PLNLTANGGL 1320
GPINIPINIT SAPGFGNSTT TPSSGFFNSG DGSASGFGNV GPGISGLWNQ VPNALQGGVS 1380

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<212> Type : PRT
<211> Length : 1436
SequenceName : SEQ ID 140
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :

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GNHLTGIGGL NSGTGNIGLF NSGTGNVGFF NSGTGNFGVF NSGNYNTGVG NAGTASTGLF  360
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TVNLGPLVVP DIVIPAFGGG IGIPINIGPL TITPITLFAQ QTFVNQLPFP TFSLGKITIP  540
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FDIRTSAGPL NIPIIDIPAA PGFGNSTQMP SSGFFNTGAG GGSGIGNLGA GVSGLLNQAG 1860
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TGNIGIGLTG DYQTGIGGLN SGAGNLGLFN SGAGNVGFFN TGTGNFGLFN SGSFNTGVGN 3300
SGTGSTGLFN AGSFNTGVAN AGSYNTGSFN VGDTNTGGFN PGSINTGWLN AGNANTGVAN 3360
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PIDIGLPVSL TIPGFTIPGG TLIPTLPLGL ALSNGIPPVD IPAIVLDRIL LDLHADTTIG 3600
PINVPIAGFG GAPGFGNSTT LPSSGFFNTG AGGGSGFSNT GAGMSGLLNA MSDPLLGSAS 3660
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<212> Type : PRT
<211> Length : 3716
SequenceName : SEQ ID 141
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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AFLNALFAGP AKMLRLNAGL GNVGNYNVGL GNVGIFNLGA ANVGAQNLGA ANAGSGNFGF 240
GNIGNANFGF GNSGLGLPPG MGNIGLGNAG SSNYGLANLG VGNIGFANTG SNNIGIGLTG 300
DNLTGIGGLN SGTGNLGLFN SGTGNIGFFN SGTGNFGVFN SGSYNTGVGN AGTASTGLFN 360
VGGFNTGVAN VGSYNTGSFN AGNTNTGGFN PGNVNTGWLN TGNTNTGIAN SGNVNTGAFI 420
SGNFSNGVLW RGDYEGLWGL SGGSTIPAIP IGLELNGGVG PITVLPIQIL PTIPLNIHQT 480
FSLGPLVVPD IVIPAFGGGT AIPISVGPIT ISPITLFPAQ NFNTTFPVGP FFGLGVVNIS 540
GIEIKDLAGN VTLQLGNLNI DTRINQSFPV TVNWSTPAVT IFPNGISIPN NPLALLASAS 600
IGTLGFTIPG FTIPAAPLPL TIDIDGQIDG FSTPPITIDR IPLNLGASVT VGPILINGVN 660
IPATPGFGNT TTAPSSGFFN SGDGGVSGFG NFGAGSSGWW NQAQTEVAGA GSGFANFGSL 720
GSGVLNFGSG VSGLYNTGGL PPGTPAVVSG IGNVGEQLSG LSSAGTALNQ SLIINLGLAD 780
VGSVNVGFGN VGDFNLGAAN IGDLNVGLGN VGGGNVGFGN IGDANFGLGN AGLAAGLAGV 840
GNIGLGNAGS GNVGFGNMGV GNIGFGNTGT NNLGIGLTGD NQTGIGGLNS GAGNIGLFNS 900
GTGNVGLFNS GTGNFGLFNS GSFNTGIGNG GTGSTGLFNA GNFNTGVANP GSYNTGSFNV 960
GDTNTGGFNP GSINTGWFNT GNANTGVANS GNVDTGALMS GNFSNGILWR GNFEGLFGLN 1020
VGITIPEFPI HWTSTGGIGP IIIPDTTILP PIHLGLTGQA NYGFAVPDIP IPAIHIDFDG 1080
AADAGFTAPA TTLLSALGIT GQFRFGPITV SNVQLNPFNV NLKLQFLHDA FPNEFPDPTI 1140
SVQIQVAIPL TSATLGGLAL PLQQTIDAIE LPAISFSQSI PIDIPPIDIP ASTINGISMS 1200
EVVPIDVSVD IPAVTITGTR IDPIPLNFDV LSSAGPINIS IIDIPALPGF GNSTELPSSG 1260
FFNTGGGGGS GIANFGAGVS GLLNQASSPM VGTLSGLGNA GSLASGVLNS GVDISGMFNV 1320
STLGSAPAVI SGFGNLGNHV SGVSIDGLLA MLTSGGSGGS GQPSIIDAAI AELRHLNPLN 1380
IVNLGNVGSY NLGFANVGDV NLGAGNLGNL NLGGGNLGGQ NLGLGNLGDG NVGFGNLGHG 1440
NVGFGNSGLG ALPGIGNIGL GNAGSNNVGF GNMGLGNIGF GNTGTNNLGI GLTGDNQTGF 1500
GGLNSGAGNL GLFNSGTGNI GFFNTGTGNW GLFNSGSYNT GIGNSGTGST GLFNAGSFNT 1560
GLANAGSYNT GSLNAGNTNT GGFNPGNVNT GWFNAGHTNT GGFNTGNVNT GAFNSGSFNN 1620
GALWTGDHHG LVGFSYSIEI TGSTLVDINE TLNLGPVHID QIDIPGMSLF DIHELVNIGP 1680
FRIEPIDVPA VVLDIHETMV IPPIVFLPSM TIGGQTYTIP LDTPPAPAPP PFRLPLLFVN 1740
ALGDNWIVGA SNSTGMSGGF VTAPTQGILI HTGPSSATTG SLALTLPTVT IPTITTSPIP 1800
LKIDVSGGLP AFTLFPGGLN IPQNAIPLTI DASGVLDPIT IFPGGFTIDP LPLSLALNIS 1860
VPDSSVPIII VPPTPGFGNA TATPSSGFFN SGAGGVSGFG NFGAGSSGWW NQAHAALAGA 1920
GSGVLNVGTL NSGVLNVGSG ISGLYNTAIV GLGTPALVSG AGNVGQQLSG VLAAGTALTQ 1980
SPIINLGLAD VGNYNLGLGN VGDFNLGAAN LGDLNLGLGN IGNANVGFGN IGHGNVGFGN 2040
SGLGAALGIG NIGLGNAGST NVGLANMGVG NIGFANTGTN NLGIGLTGDN QTGIGGLNSG 2100
AGNIGLFNSG TGNIGFFNSG TGNWGLFNSG SFNTGIGNSG TGSTGLFNAG GFTTGLANAG 2160
SYNTGSFNVG DTNTGGFNPG SINTGWFNTG NANTGIANSG NVDTGALMSG NFSNGILWRG 2220
NYEGLFSYSY SLDVPRITIL DAHFTGAFGP VVVPPIPVLA INAHLTGNAA MGAFTIPQID 2280
IPALNPNVTG SVGFGPIAVP SVTIPALTAA RAVLDMAASV GATSEIEPFI VWTSSGAIGP 2340
TWYSVGRIYN AGDLFVGGNI ISGIPTLSTT GPVHAVFNAA SQAFNTPALN IHQIPLGFQV 2400
PGSIDAITLF PGGLTFPANS LLNLDVFVGT PGATIPAITF PEIPANADGE LYVIAGDIPL 2460
INIPPTPGIG NTTTVPSSGF FNTGAGGGSG FGNFGANMSG WWNQAHTALA GAGSGIANVG 2520
TLHSGVLNLG SGLSGIYNTS TLPLGTPALV SGLGNVGDHL SGLLASNVGQ NPITIVNIGL 2580
ANVGNGNVGL GNIGNLNLGA ANIGDVNLGF GNIGDVNLGF GNIGGGNVGF GNIGDANFGF 2640
GNSGLAAGLA GMGNIGLGNA GSGNVGWANM GLGNIGFGNT GTNNLGIGLT GDNQSGIGGL 2700
NSGTGNIGLF NSGTGNIGFF NSGTANFGLF NSGSYNTGIG NSGVASTGLV NAGGFNTGVA 2760
NAGSYNTGSF NAGDTNTGGF NPGSTNTGWF NTGNANTGVA NAGNVNTGAL ITGNFSNGIL 2820
WRGNYEGLAG FSFGYPIPLF PAVGADVTGD IGPATIIPPI HIPSIPLGFA AIGHIGPISI 2880
PNIAIPSIHL GIDPTFDVGP ITVDPITLTI PGLSLDAAVS EIRMTSGSSS GFKVRPSFSF 2940
FAVGPDGMPG GEVSILQPFT VAPINLNPTT LHFPGFTIPT GPIHIGLPLS LTIPGFTIPG 3000
GTLIPQLPLG LGLSGGTPPF DLPTVVIDRI PVELHASTTI GPVSLPIFGF GGAPGFGNDT 3060

TAPSSGFFNT GGGGGSGFSN SGSGMSGVLN AISDPLLGSA SGFANFGTQL SGILNRGAGI 3120
SGVYNTGTLG LVTSAFVSGF MNVGQQLSGL LFAGTGP 3157
<212> Type : PRT
<211> Length : 3157
SequenceName : SEQ ID 142
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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SSVAMAAAAA PYAGWLSAAA ASAESAAGQA RAVVGVFEAA LAETVDPFVI AANRSRLVSL 120
ALSNLFGQNT PAIAAAEFDY ELMWAQDVAA MLGYHTGASA AAEALAPFGS PLASLAAAAE 180
PAKSLAVNLG LANVGLFNAG SGNVGSYNVG AGNVGSYNVG GGNIGGNNVG LGNVGWGNFG 240
LGNSGLTPGL MGLGNIGFGN AGSYNFGLAN MGVGNIGFAN TGSGNFGIGL TGDNLTGFGG 300
FNTGSGNVGL FNSGTGNVGF FNSGTGNWGV FNSGSYNTGI GNSGIASTGL FNAGGFNTGV 360
VNAGSYNTGS FNAGEANTGG FNPGSVNTGW LNTGDINTGV ANSGDVNTGA FISGNYSNGV 420
LWRGDYQGLL GFSSGANVLP VIPLSLDING GVGAITIEPI HILPDIPINI NETLYLGPLV 480
VPPINVPAIS LGVGIPNISI GPIKINPITL WPAQNFNQTI TLAWPVSSIT IPQIQQVALS 540
PSPIPTTLIG PIHINTGFSI PVTFSYSTPA LTLFPVGLSI PTGGPLTLTL GVTAGTEAFT 600
IPGFSIPEQP LPLAINVIGH INALSTPAIT IDNIPLNLHA IGGVGPVDIV GGNVPASPGF 660
GNSTTAPSSG FFNTGAGGVS GFGNVGAHTS GWFNQSTQAM QVLPGTVSGY FNSGTLMSGI 720
GNVGTQLSGM LSGGALGGNN FGLGNIGFDN VGFGNAGSSN FGLANMGIGN IGLANTGNGN 780
IGIGLSGDNL TGFGGFNSGS ENVGLFNSGT GNVGFFNSGT GNLGVFNSGS HNTGFFLTGN 840
NINVLAPFTP GTLFTISEIP IDLQVIGGIG PIHVQPIDIP AFDIQITGGF IGIREFTLPE 900
ITIPAIPIHV TGTVGLEGFH VNPAFVLFGQ TAMAEITADP VVLPDPFITI DHYGPPLGPP 960
GAKFPSGSFY LSISDLQING PIIGSYGGPG TIPGPFGATF NLSTSSLALF PAGLTVPDQT 1020
PVTVNLTGGL DSITLFPGGL AFPENPVVSL TNFSVGTGGF TVFPQGFTVD RIPVDLHTTL 1080
SIGPFPFRWD YIPPTPANGP IPAVPGGFGL TSGLFPFHFT LNGGIGPISI PTTTVVDALN 1140
PLLTVTGNLE VGPFTVPDIP IPAINFGLDG NVNVSFNAPA TTLLSGLGIT GSIDISGIQI 1200
TNIQTQPAQL FMSVGQTLFL FDFRDGIELN PIVIPGSSIP ITMAGLSIPL PTVSESIPLN 1260
FSFGSPASTV KSMILHEILP IDVSINLEDA VFIPATVLPA IPLNVDVTIP VGPINIPIIT 1320
EPGSGNSTTT TSDPFSGLAV PGLGVGLLGL FDGSIANNLI SGFNSAVGIV GPNVGLSNLG 1380
GGNVGLGNVG DFNLGAGNVG GFNVGGGNIG GNNVGLGNVG FGNVGLANSG LTPGLMGLGN 1440
IGFGNAGSYN FGLANMGVGN IGFANTGSGN FGIGLTGDNL TGFGGFNTGS GNVGLFNSGT 1500
GNVGFFNSGT GNWGVFNSGS YNTGIGNSGI ASTGLFNAGG FNTGVVNAGS YNTGSFNAGQ 1560
ANTGGFNPGS VNTGWLNTGD INTGVANSGD VNTGAFISGN YSNGAFWRGD YQGLLGFSYR 1620
PAVLPQTPFL DLTLTGGLGS VVIPAIDIPA IRPEFSANVA IDSFTVPSIP IPQIDLAATT 1680
VSVGLGPITV PHLDIPRVPV TLNYLFGSQP GGPLKIGPIT GLFNTPIGLT PLALSQIVIG 1740
ASSSQGTITA FLANLPFSTP VVTIDEIPLL ASITGHSEPV DIFPGGLTIP AMNPLSINLS 1800
GGTGAVTIPA ITIGEIPFDL VAHSTLGPVH ILIDLPAVPG FGNTTGAPSS GFFNSGAGGV 1860
SGFGNVGAMV SGGWNQAPSA LLGGGSGVFN AGTLHSGVLN FGSGMSGLFN TSVLGLGAPA 1920
LVSGLGSVGQ QLSGLLASGT ALHQGLVLNF GLADVGLGNV GLGNVGDFNL GAGNVGGFNV 1980
GGGNIGGNNV GLGNVGWGNF GLGNSGLTPG LMGLGNIGFG NAGSYNFGLA NMGVGNIGFA 2040
NTGSGNFGIG LTGDNLTGFG GFNTGSGNVG LFNSGTGNVG FFNSGTGNWG VFNSGSYNTG 2100
IGNSGIASTG LFNAGGFNTG VVNAGSYNTG SFNAGQANTG GFNPGSVNTG WLNTGDINTG 2160
VANSGDVNTG AFISGNYSNG AFWRGDYQGL LGFSYTSTII PEFTVANIHA SGGAGPIIVP 2220
SIQFPAIPLD LSATGHIGGF TIPPVSISPI TVRIDPVFDL GPITVQDITI PALGLDPATG 2280
VTVGPIFSSG SIIDPFSLTL LGFINVNVPA IQTAPSEILP FTVLLSSLGV THLTPEITIP 2340
GFHIPVDPIH VELPLSVTIG PFVSPEITIP QLPLGLALSG ATPAFAFPLE ITIDRIPVVL 2400
DVNALLGPIN AGLVIPPVPG FGNTTAVPSS GFFNIGGGGG LSGFHNLGAG MSGVLNAISD 2460
PLLGSASGFA NFGTQLSGIL NRGADISGVY NTGALGLITS ALVSGFGNVG QQLAGLIYTG 2520
TGP 2523
<212> Type : PRT
<211> Length : 2523
SequenceName : SEQ ID 143
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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SYQAFGAQLS AFHAQFVQSL TNGARSYVVA EATSAAPLQD LLGVVNAPAQ ALLGRPLIGN 120
GANGADGTGA PGGPGGLLLG NGGNGGSGAP GQPGGAGGDA GLIGNGGTGG KGGDGLVGSG 180
AAGGVGGRGG WLLGNGGTGG AGGAAGATLV GGTGGVGGAT GLIGSGGFGG AGGAAAGVGT 240

TGGVGGSGGV GGVFGNGGFG GAGGLGAAGG VGGAASYFGT GGGGGVGGDG APGGDGGAGP 300
LLIGNGGVGG LGGAGAAGGN GGAGGMLLGD GGAGGQGGPA VAGVLGGMPG AGGNGGNANW 360
FGSGGAGGQG GTGLAGTNGV NPGSIANPNT GANGTDNSGN GNQTGGNGGP GPAGGVGEAG 420
GVGGQGGLGE SLDGNDGTGG KGGAGGTAGT DGGAGGAGGA GGIGETDGSA GGVATGGEGG 480
DGATGGVDGG VGGAGGKGGQ GHNTGVGDAF GGDGGIGGDG NGALGAAGGN GGTGGAGGNG 540
GRGGMLIGNG GAGGAGGTGG TGGGGAAGFA GGVGGAGGEG LTDGAGTAEG GTGGLGGLGG 600
VGGTGGMGGS GGVGGNGGAA GSLIGLGGGG GAGGVGGTGG IGGIGGAGGN GGAGGAGTTT 660
GGGATIGGGG GTGGVGGAGG TGGTGGAGGT TGGSGGAGGL IGWAGAAGGT GAGGTGGQGG 720
LGGQGGNGGN GGTGATGGQG GDFALGGNGG AGGAGGSPGG SSGIQGNMGP PGTQGADG 778

<212> Type : PRT
<211> Length : 778
SequenceName : SEQ ID 144
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
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QQGNGGNGGN GGTGGKGGTG GDGALAGSSG GAGGKGGNGG DAGKAGTGSA PGTAGTGGDG 120
GKGGNGGIGA AGTTGPVGTG ASGGTGGSGG AGGTGGDGGA ANGGTAGAGG AGGNGGKGGD 180
GGAGVTSSTA GNSGGAGGSG GKGGDAGAGG AGATPGANGI AGNGGDGGDG AAGAVGISGA 240
TGAGDGGHGG TGAAGGNGGT GGAGGSGIDG VGGGTGGTGG NGGNGAIGGA GGDAGGSGNS 300
GGNGGIGGKG GNAGAGGAAG SNGGTVGANG TGGDGGNGGA AGAATAGSNG GAGTGSAGGN 360
GGTGGRGGSG GAGGDGIGGV GGGKGGNGAD GEVGGAGGAG GSGPNTSPGG NGGQGGQGGS 420
GGAGGAAGAG GAGGGANGTA GNGGQGGAGG TGGAGAASSA TNGGSGGAGG TGGDGGSGGA 480
GGTGGAGGTG GAAGDGGQGG QGGAGGGAGG QGGAGGAGGT GGNGGNITGG TAGTAGAAGN 540
GGAAGKGGAG GQGGTGGGTG GQGGAGGDGG AGGTGGDRTV GGGTVPAGSG GQGGNAGGGG 600
AGGQGGADGG SGGDGGDAGT GGNGGNGGNR NSGNGTGGAG GNGGGGANGG AGGAGGSGGG 660
TGGNGGAGGD AGDAGNGGNG NGTGNGGNGG NGGIAGMGGN GGAGTGSGNG GNGGSGGNGG 720
NAGMGGNSGT GSGDGGAGGN GGAAGTGGTG GDGGLTGTGG TGGSGGTGGD GGNGGNGADN 780
TANMTAQAGG DGGNGGDGGF GGGAGAGGGG LTAGANGTGG QGGAGGDGGN GAIGGHGPLT 840
DDPGGNGGTG GNGGTGGTGG AGIGSLGGGT GGDGGNGGNG GTGGEGGEVG GAGGTGGAAG 900
NGGDGGTGGT GGGDGGAGGT GGTGGTGGLG DPRVGGSGGD GGTGGSGGAA GNGGNGGNAG 960
AGGNGNGGTG GAGGIGGTGG NGGDAEPGVP PGAGGAGGAG TTGGKGGTGG NGSGTGSGGT 1020
GGDGGTGGGG GNGGTGWNGG KGDTGSGGGA GDGGKAPAGG TGGAGGDGGA GGKGGSGGV 1079

<212> Type : PRT
<211> Length : 1079
SequenceName : SEQ ID 145
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
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QEYQALSARV ATFHEQFVRS LTAAGSAYAT AEAANASPLQ ALEQQVLGAI NAPTQLWLGR 120
PLIGDGVHGA PGTGQPGGAG GLLWGNGGNG GSGAAGQVGG PGGAAGLFGN GGSGGSGGAG 180
AAGGVGGSGG WLNGNGGAGG AGGTGANGGA GGNAWLFGAG GSGGAGTNGG VGGSGGFVYG 240
NGGAGGIGGI GGIGGNGGDA GLFGNGGAGG AGAAGLPGAA GLNGGDGSDG GNGGTGGNGG 300
RGGLLVGNGG AGGAGGVGGD GGKGGAGDPS FAVNNGAGGN GGHGGNPGVG GAGGAGGLLA 360
GAHGAAGATP TSGGNGGDGG IGATANSPLQ AGGAGGNGGH GGLVGNGGTG GAGGAGHAGS 420
TGATGTALQP TGGNGTNGGA GGHGGNGGNG GAQHGDGGVG GKGGAGGSGG AGGNGFDAAT 480
LGSPGADGGM GGNGGKGGDG GKAGDGGAGA AGDVTLAVNQ GAGGDGGNGG EVGVGGKGGA 540
GGVSANPALN GSAGANGTAP TSGGNGGNGG AGATPTVAGE NGGAGGNGGH GGSVGNGGAG 600
GAGGNGVAGT GLALNGGNGG NGGIGGNGGS AAGTGGDGGK GGNGGAGANG QDFSASANGA 660
NGGQGGNGGN GGIGGKGGDA FATFAKAGNG GAGGNGGNVG VAGQGGAGGK GAIPAMKGAT 720
GADGTAPTSG GDGGNGGNGA SPTVAGGNGG DGGKGGSGGN VGNGGNGGAG GNGAAGQAGT 780
PGPTSGDSGT SGTDGGAGGN GGAGGAGGTL AGHGGNGGKG GNGGQGGIGG AGERGADGAG 840
PNANGANGEN GGSGGNGGDG GAGGNGGAGG KAQAAGYTDG ATGTGGDGGN GGDGGKAGDG 900
GAGENGLNSG AMLPGGGTVG NPGTGGNGGN GGNAGVGGTG GKAGTGSLTG LDGTDGITPN 960
GGNGGNGGNG GKGGTAGNGS GAAGGNGGNG GSGLNGGDAG NGGNGGGALN QAGFFGTGGK 1020
GGNGGNGGAG MINGGLGGFG GAGGGGAVDV AATTGGAGGN GGAGGFASTG LGGPGGAGGP 1080
GGAGDFASGV GGVGGAGGDG GAGGVGGFGG QGGIGGEGRT GGNGGSGGDG GGGISLGGNG 1140
GLGGNGGVSE TGFGGAGGNG GYGGPGGPEG NGGLGGNGGA GGNGGVSTTG GDGGAGGKGG 1200

NGGDGGNVGL GGDAGSGGAG GNGGIGTDAG GAGGAGGAGG NGGSSKSTTT GNAGSGGAGG 1260
NGGTGLNGAG GAGGAGGNAG VAGVSFGNAV GGDGGNGGNG GHGGDGTTGG AGGKGGNGSS 1320
GAASGSGVVN VTAGHGGNGG NGGNGGNGSA GAGGQGGAGG SAGNGGHGGG ATGGDGGNGG 1380
NGGNSGNSTG VAGLAGGAAG AGGNGGGTSS AAGHGGSGGS GGSGTTGGAG AAGGNGGAGA 1440
GGGSLSTGQS GGPRRQRWCR WQRRRWLGRQ RRRRWCRWQR RCRRQRWRWR CRQRRLRRQW 1500
RQGRRRCRPW LHRRRGRQGR RWRQRRFQQR QRSRWQRR 1538
<212> Type : PRT
<211> Length : 1538
SequenceName : SEQ ID 146
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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DYQTLSVQVT AFHVQFAQTL TNAGQLYAVV DVGNGVLLKT EQQVLGVINA PTQTLVGRPL 120
IGDGTHGAPG TGQNGGAGGI LWGNGGNGGS GAPGQPGGRG GDAGLFGHGG HGGVGGPGIA 180
GAAGTAGLPG GNGANGGSGG IGGAGGAGGN GGLLFGNGGA GGQGGSGGLG GSGGTGGAGM 240
AAGPAGGTGG IGGIGGIGGA GGVGGHGSAL FGHGGINGDG GTGGMGGQGG AGGNGWAAEG 300
ITVGIGEQGG QGGDGGAGGA GGIGGSAGGI GGSQGAGGHG GDGGQGGAGG SGGVGGGGAG 360
AGGDGGAGGI GGTGGNGSIG GAAGNGGNGG RGGAGGMATA GSDGGNGGGG GNGGVGVGSA 420
GGAGGTGGDG GAAGAGGAPG HGYFQQPAPQ GLPIGTGGTG GEGGAGGAGG DGGQGDIGFD 480
GGRGGDGGPG GGGGAGGDGS GTFNAQANNG GDGGAGGVGG AGGTGGTGGV GADGGRGGDS 540
GRGGDGGNAG HGGAAQFSGR GAYGGEGGSG GAGGNAGGAG TGGTAGSGGA GGFGGNGADG 600
GNGGNGGNGG FGGINGTFGT NGAGGTGGLG TLLGGHNGNI GLNGATGGIG STTLTNATVP 660
LQLVNTTEPV VFISLNGGQM VPVLLDTGST GLVMDSQFLT QNFGPVIGTG TAGYAGGLTY 720
NYNTYSTTVD FGNGLLTLPT SVNVVTSSSP GTLGNFLSRS GAVGVLGIGP NNGFPGTSSI 780
VTAMPGLLNN GVLIDESAGI LQFGPNTLTG GITISGAPIS TVAVQIDNGP LQQAPVMFDS 840
GGINGTIPSA LASLPSGGFV PAGTTISVYT SDGQTLLYSY TTTATNTPFV TSGGVMNTGH 900
VPFAQQPIYV SYSPTAIGTT TFN 923
<212> Type : PRT
<211> Length : 923
SequenceName : SEQ ID 147
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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GAGGAGGSGG SGAAGGAGGA GGAGGLFASG GSGGFGGFAS TGTGGAGGTG GAGGLFASGG 120
VGGTGGGAGS GGTGGVGGTG GAGGLFASGG AGGAGGSGGT GGAGGTGGAG GLFGAGGAGG 180
LGGQGNHTGG HGGAGGSAGL LALGDGGAGG AGGAATTGTG GAGGAGGKAG LLFGSGGAGG 240
SGGAAGTFGD TGNSGGAGGA GGKAGLLFGS GGAGGSGGAG GFANGSTGGA GGAGGGAGLI 300
GNGGNGGSGG TSVATGGAGN GGAGGAGGGA GLIGNGGNGG SGGMGDAPGG TGVGGIGGLL 360
LGLDGANAPA STNPLHTAQQ QALAAVNAPI QAVTGRPLIG NGANGAPGSG APGGHGGWLF 420
GGGGTGGSGV SGGAGGDGGA GGILFGAGGA GGAGGAVTGT GATGGSGGAG GGALLFGAGG 480
AGGAGGSSGI GGFAAGGAGG PGGAGGLFNG GGAGGAGGSG VSGGAGGEGG AGGAGGLFAG 540
GGAGGAGGSG NNVGGAGGAG GVGGLFGAGG AGGSGGGGSV AGDSGAGGNA GLLAPGLAGG 600
AGGGGGQGFD TGGAGGPGGD AGLLVGSGGV GGAGGFGLTT GGPGAAGGDA GLLFGSGGAG 660
GAGGSGRTDL GGAGGAGGKA GLIGNGGNGG AGGAGGNGGG DGGPGGAAFG LGNGGNGGNG 720
GTGTSAGSPG AGGAGGSLIG AEGLPGLLP 749
<212> Type : PRT
<211> Length : 749
SequenceName : SEQ ID 148
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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AYQTVSAQAS AFHAQFVQAL TGGGGAYAAA EAANVSAAQS TDQRLLDLIN GPTQALLGRP 120
LIGDGANGGP GQDGGPGGLL YGNGGNGGTS TTAGVAGGNG GAAGLIGNGG AGGGGGAGAA 180
GGNGGAGGWL YGNGGAGGAG GTSVIPGVAG GNGGAGGSAG LWGTGGAGGD GGNGRSGPVN 240
VAGSAGGNGG AGGAAGLFGD AGAGGNGGKG GAGGAAFSIN FTAGDGGAGG AGGSGGHALL 300

WGAGGAGGNG GSGGTGGAGG STAGAGGNGG AGGGGGTGGL LFGNGGAGGH GAAAGNGLAA 360
GNGVSSSGGG GAGGTGGAGG DGGAGGAGGN ARLWGVGGAG GAGGDGGAGG AGGKGGSGLS 420
GNANGGAGGD SGRGGTGGAG GEGGAAGLLV GTGGHGGDGG AGGAAVKGGD GGAAAGTGIA 480
GAGGRGGAGG SGGSGGDGGG GAAGPAGWLF GDGGAGGNGG AAAAGGAGGQ AGGGGGNGGN 540
GGNGGNGGNG GNGATGGWLY GNGGAGGQGA TAGAGGAGAN GVSSTNGGGT GGNGGIGGTG 600
GSGGAGGNAG LLGVGGAGGH GASGGAGDRG GAGGTGFISS DGGAGGDGGD GGNGGAGGTG 660
GLLFGAGGNG GPGGSGGAAD IGGNGGAGNG GGTDGNGGNG GSGGGAGSGG DGGGAGGNGA 720
WLFGNGGAGG GGGKGGNGAG GGLGGGSFGL PGLNGSGGDG GDGGNGAPGG VLYGNGGAGG 780
QGSSGGIGGP GATGGAGGKG GDGGDAQLIG DGGNGGNGGA GGTGGTPGPG GPGGSGGLGG 840
LLFGQTGTAG VSP 853
<212> Type : PRT
<211> Length : 853
SequenceName : SEQ ID 149
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSYLVVVPEL VAAAATDLAN IGSSISAANA AAAAPTTALV AAGGDEVSAA IAALFGAHAR 60
AYQALSAQAA MFHEQFVRAL AAGGNSYAVA EAATAQSVQQ DLLNLINAPT QALLGRPLIG 120
NGANGLPGTG QNGGDGGILY GNGGNGGSGG VNQAGGNGGN AGLWGNGGSG GAGGNATTAG 180
RNGFNGGAGG SGGLLWGNGG AGGAGGNGGP APLVGGVGTT GGAGGNGGGA GLFYGFGGAG 240
GNGGMGGVAP STGPSMGILP AGGVGGPGGS GGASALAFGS GGVGGAGGLG GPTDGTVQGV 300
GGFGGQGGNG GQSGLLFGNA GAGGAGAAGG AGTGDTESFG GHGGAGGDGG AVGLIGNGGA 360
GGTGSPGAVV GGNGGVGGLG GAGSPGGLLY GTGGAGGNGG PGGDGGTGAT VGFAGSGGFG 420
GAGGIAQLFG TGGMGGSGGG IGAGTTTVVP PDVAPVGGTG GNGGRAGLLL GVGGMGGNGG 480
ATSVGGTLYA AGGNGGDGGL VWGNGGTGGS GGAGGAGSVG NGGAGGNAAL LFGNGGAGGA 540
GGAGGIGAGG AGGFGAVLFG NGGAGGSGAP GGIGAGGNGG NALLVGNGGN GGAGTGGAAG 600
GAGGSGGLLF GQNGMPGP 618
<212> Type : PRT
<211> Length : 618
SequenceName : SEQ ID 150
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MNFSVLPPEI NSALIFAGAG PEPMAAAATA WDGLAMELAS AAASFGSVTS GLVGGAWQGA 60
SSSAMAAAAA PYAAWLAAAA VQAEQTAAQA AAMIAEFEAV KTAVVQPMLV AANRADLVSL 120
VMSNLFGQNA PAIAAIEATY EQMWAADVSA MSAYHAGASA IASALSPFSK PLQNLAGLPA 180
WLASGAPAAA MTAAAGIPAL AGGPTAINLG IANVGGGNVG NANNGLANIG NANLGNYNFG 240
SGNFGNSNIG SASLGNNNIG FGNLGSNNVG VGNLGNLNTG FANTGLGNFG FGNTGNNNIG 300
IGLTGNNQIG IGGLNSGTGN FGLFNSGSGN VGFFNSGNGN FGIGNSGNFN TGGWNSGHGN 360
TGFFNAGSFN TGMLDVGNAN TGSLNTGSYN MGDFNPGSSN TGTFNTGNAN TGFLNAGNIN 420
TGVFNIGHMN NGLFNTGDMN NGVFYRGVGQ GSLQFSITTP DLTLPPLQIP GISVPAFSLP 480
AITLPSLNIP AATTPANITV GAFSLPGLTL PSLNIPAATT PANITVGAFS LPGLTLPSLN 540
IPAATTPANI TVGAFSLPGL TLPSLNIPAA TTPANITVGA FSLPGLTLPS LNIPAATTPA 600
NITVGAFSLP GLTLPSLNIP AATTPANITV SGFQLPPLSI PSVAIPPVTV PPITVGAFNL 660
PPLQIPEVTI PQLTIPAGIT IGGFSLPAIH TQPITVGQIG VGQFGLPSIG WDVFLSTPRI 720
TVPAFGIPFT LQFQTNVPAL QPPGGGLSTF TNGALIFGEF DLPQLVVHPY TLTGPIVIGS 780
FFLPAFNIPG IDVPAINVDG FTLPQITTPA ITTPEFAIPP IGVGGFTLPQ ITTQEIITPE 840
LTINSIGVGG FTLPQITTPP ITTPPLTIDP INLTGFTLPQ ITTPPITTPP LTIDPINLTG 900
FTLPQITTPP ITTPPLTIEP IGVGGFTTPP LTVPGIHLPS TTIGAFAIPG GPGYFNSSTA 960
PSSGFFNSGA GGNSGFGNNG SGLSGWFNTN PAGLLGGSGY QNFGGLSSGF SNLGSGVSGF 1020
ANRGILPFSV ASVVSGFANI GTNLAGFFQG TTS 1053
<212> Type : PRT
<211> Length : 1053
SequenceName : SEQ ID 151
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MLYVVASPDL MTAAATNLAE IGSAISTANG AAALPTVEVV AAAADEVSTQ IAALFGAHAR 60

SYQTLSTQAA AFHSRFVQAL TTAAASYASV EAANASPLQV ALDVINAPAQ TLLGRPLIGN 120
GADGSTPGQA GGPGGLLYGN GGNGAAGGPN QAGGAGGNAG LIGNGGAGGA GGVGAVGGKR 180
GTGGLLFGNG GAGGQGGLGL AGINGGSGGQ GGHGGNAILF GQGGAGGPGG TGAMGVAGTN 240
PTPIGTAAPG SDGVNQIGNG GNTDLTGGAG GDGNAGSTTV NGGNGGTGGA ARNSSGGTGN 300
SFGGAGGAGG DGANGGDGGA GGEALTEGGA TAVSGAGGKG GNAEASGGAG GNGGKGGFAQ 360
ATTSVTGGNG GNGGNGHDSN APGGAGGSGG VGGDGGRGGL LAGNGGTGGA GGNGGTGGAG 420
APGGAGGAGG KADIANSLGD NATVTGGNGG TGGDGGSALG TGGAGGAGGL GGHGGAGGLL 480
IGNGGAGGAG GLGGAGGAGG AGGEGGAGGA GGEAIPGGAS TNSAGGDGGA GGTGGNGGDG 540
GAGGAPGLGG AGGAGGWLIG QSGSTGGGGA GGAGGAGGAG GAGGSGGAGG HGDTTSGKNG 600
SSGTAGFDGN PGQPG 615
<212> Type : PRT
<211> Length : 615
SequenceName : SEQ ID 152
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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SSVAMAAAAA PYAGWLAAAA TQAEQAATQA QVMVAEFEAV RLAMVQPALV AANRSGLISL 120
VISNLFGQNA PAIAAAEAAY EEMWALDVSA MAAYHSGASA VAVALPAFAL PLRLPAGLAA 180
GPAAVVTALT TAVGMPTFAG RAIAASLGLA NVGGGNLGNA NNGLGNIGNA NLGNNNLGSG 240
NFGSFNIGSA NLGGNNIGIG NAGANNFGLA NLGNLNTGFA NAGIGNFGIA NTGNNNIGNG 300
LTGNNQIGIG GLNSGNGNVG LFNAGSANIG FFNSGNGNFG IGNSGNFSTG LFNPGHGNTG 360
FLNAGSFNTG MFDVGNANTG SFNVGHYNFG AFNPGPSNTG TFNTGGANTG WFNTGSINTG 420
AFNIGDMNNG LFNTGDMNNG VFYRGVGQGS LQFAITSPDL TLPSLEIPGI SVPAFSLPAI 480
TLPSLTIPAV TTPANVTVGA FDLPGLTVPS LTIPAAMTPA NITVGAFDLP GLTVPSLTIP 540
ATTTPANITV GAFNLPQLSI PSVTVPPITI PAGTALGAFN LPTLSIPSVT VPPITIPAGT 600
TVGGFTLPTI HTPLISTPQI SIGGFSTPGI ATQANSGVIN LPTFSLNGIT ITNLVVFIPN 660
NITALQTNMP GVFPQIGGFA NTPPAFINTG TITVGGGQIN GVGFSIGAIN VTPFTLPNVV 720
IQPWSLGGIS VDGFTLPEIS TQEFTTPALT ISPIGVGALS LPDITTQQFT TPELTIDPIT 780
LGGFTLPQLS IPAITTPAFT IDPIALGGFT LPQIMTPEIT TPPFAIDPIG LSGFTLPQVN 840
IPEITTPEFT IQPVGLAAFT TPALTIASIH LPSTTMGGFA IPAGPGYFNS SATPSLGFFN 900
AGIGGNSGFG NSGSGLSGWF NTSPVGLLAG SGYQNYGGLI SGFSNLGSGI SGFANTGTLP 960
FAVTSLVSGL ANIGNNLSGL FFQSTTP 987
<212> Type : PRT
<211> Length : 987
SequenceName : SEQ ID 153
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
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AYQAVSAQMS AFHAQFMQAL TGAGGAYAAA EAVNVSAAQS VEQDLLAAIN ARFERIFGRP 120
LIGDGANGGP GQDGGPGGLL YGNGGNGGTS TTVGMAGGNG GAAGLIGNGG FGGGGGPGAA 180
GGNGGAGGWL FGNGGAGGAG GLGVAPGVPG GAGGAGGAGG VGGPAGLWGH GGAGGAGGAG 240
VAGAGGFEGT IGAGGAGGVG GAGGVGGAGG AGGWLYGDAG AGGDGGVGGA GGTGGLGNRG 300
GAGGAGGAGG VGGAGGAAGL WGGGGAGGVG GTGGGAGLGA QSVTFSSSLS GLSGGDGGAG 360
GAGGAGGAGG TGGWLYGGGG AAGSGGDGGT GGQGGAGGAG VFSLFGSGGG PGGNGGVGGV 420
GGVGGAGGRA GLFGVGGLGG AGGDAGDSGE GGFGGPGLAG GLFGNPGNGG VGGIGGDAAA 480
GGAGGAGGNG GAGGNGGWLF GNGGAGGSGG DGGAAGRGGA GNLGSAGGIN APAGNPGSGS 540
VGIGGAGGAG GTAGLFGDGG AGGAGGAGAA GGFGGISAAT PSAGSEGAMG GAGGVGGNAR 600
LLGTGGAGGV GGGGAGGDG GRGGVATPGG QGGDAGDGGA GGAGGNGGGA SGAGGWLLGT 660
GGAGGAGGNG GNGGKAGFSP GPTNFGLNGA GGGGGVGGNG ATGPWLFGDG GPTPGSTGAG 720
AAGGHGGDAQ LIGNGGHGGA GGTGVPNGSG GAGGLSGLLF GEPGANG 767
<212> Type : PRT
<211> Length : 767
SequenceName : SEQ ID 154
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :

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AYQALSAQAT IFHDQFVQAL TSGGNLYAAA ESHTVEQMVL NAINAPTQTL FGRPLIGDGA 120
NGTAENPDGQ NGGLLFGNGG NGFTQTTAGV AGGNGGSAGL IGNGGAGGGG GAGAAGGLGG 180
NGGWLYGNGG AGGIGGAGTG TGGHGGAGGA GGRAWLWGTG GAGGAGGDGG WLFGDGGAGG 240
TGGNGGSGFN SLTSSVGGAG GAGGHAGLFG AGGTGGTGGI GGQNTETGPA ASNGGAGGAG 300
GGGGYLVGDG GAGGTGGAGG KNSSGGATLT GGTGGTGGAG GAAGWLYGSG GAGGAGGAGG 360
LNNAGGATGG TGGTGGAGGS GAWLYGNGGA AGAGGNGGNN TSAGTGGVGA SGGTGGNAGL 420
IGAGGHGGAG GAGGNQTGGV GNGGAGGNGG AGGAGGQLYG NGGDGGNGGA GGANIAGGNG 480
SDGGAAGHGG AGGSARLIGA GGHGGDGGAG GNTAGRRADA IAGTGGDGGN GGNGGLLSGN 540
AGAGGHGGAG GSSTATTTTG TPPTGATGGN GGNGGAGGTA GFTGSGGIGG NGGAGGTGGN 600
AGVALSVGST GGLGGNGGSG GLGGGGGSLF GNGGAGGVGA TGGNGGSGIG PASVGGNGGK 660
GGVGAAGGLA GQIGNGGSGG SGGAGGNGGT GDTAGNGGNG GAGAVGGNAQ LIGNGGNGGG 720
GGNGGTGADG T 731
<212> Type : PRT
<211> Length : 731
SequenceName : SEQ ID 155
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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NNIGFGNTGS GNFGFGNTGN NNIGIGLTGD GQIGIGGLNS GSGNIGFGNS GTGNVGLFNS 120
GTGNVGFGNS GTANTGFGNA GNVNTGFWNG GSTNTGLANA GAGNTGFFDA GNYNFGSLNA 180
GNINSSFGNS GDGNSGFLNA GDVNSGVGNA GDVNTGLGNS GNINTGGFNP GTLNTGFFSA 240
MTQAGPNSGF FNAGTGNSGF GHNDPAGSGN SGIQNSGFGN SGYVNTSTTS MFGGNSGVLN 300
TGYGNSGFYN AAVNNTGIFV TGVMSSGFFN FGTGNSGLLV SGNGLSGFFK NLFG 354

<212> Type : PRT
<211> Length : 354
SequenceName : SEQ ID 156
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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AYQVASAQAA AVHAQFVEAL SAGAGAYASA EAAGAAVLAN PAQSVQQDLL AAVNAQSVAL 120
TGRPLIGNGA NGAPGTGANG APGGWLLGNG GAGGSAAAGS GLPGGAGGAA GLFGTGGAGG 180
AGGSSTVGDG EAGGAGGSGG WLLGTGGVGG VGGLGAGAGG AGGVGGAGGL LGAGGHGGAG 240
GLGAVTGGVG GTGGAGGLLA GLLAGPGGAG GTGGRGFLNN GGVGGAGGNA GLLFGAGGTG 300
GSGGAGLGGD GGAGGAGGNT GVLFGNAGSG GTGGFGDTDG GAGGAGGDAG WLGSGGVGGA 360
GGFGETGDGG VGGAGGKAGL LIGNGGAGGA GGQGAVTGGT GGAGGDGVLI GNGGNAGIGG 420
TGPTAGDTGA GGISGLLLGA DGFNTPASAS PLHTLKQQAL AAINAPTQTL TGRPLIGNGT 480
PGAVGSGATG APGGWLLGDG GAGGSGAAGS GAPGGAGGAA GLWGTGGAGG AGGSSAGGGG 540
AGGAGGAGGW LLGDGGAGGI GGASTVLGGT GGGGGVGGLW GAGGAGGAGG TGLVGGDGGA 600
GGAGGTGGLL AGLIGAGGGH GGTGGLSTNG DGGVGGAGGN AGMLAGPGGA GGAGGDGENL 660
DTGGDGGAGG SAGLLFGSGG AGGAGGFGFL GGDGGAGGNA GLLLSSGGAG GFGGFGTAGG 720
VGGAGGNAGW LGFGGAGGVG GSAGLIGTGG NGGNGGTGAN AGSPGTGGAG GLLLGQNGLN 780
GLP 783
<212> Type : PRT
<211> Length : 783
SequenceName : SEQ ID 157
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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QYQALSVQVA AFHEQFVQAL TAAAGRYAST EAAVERSLLG AVNAPTEALL GRPLIGNGAD 120
GTAPGQPGAA GGLLFGNGGN GAAGGFGQTG GSGGAAGLIG NGGNGGAGGT GAAGGAGGNG 180
GWLWGNGGNG GVGGTSVAAG IGGAGGNGGN AGLFGHGGAG GTGGAGLAGA NGVNPTPGPA 240
ASTGDSPADV SGIGDQTGGD GGTGGHGTAG TPTGGTGGDG ATATAGSGKA TGGAGGDGGT 300
AAAGGGGGNG GDGGVAQGDI ASAFGGDGGN GSDGVAAGSG GGSGGAGGGA FVHIATATST 360

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GGSGGFGGNG AASAASGADG GAGGAGGNGG AGGLLFGDGG NGGAGGAGGI GGDGATGGPG    420
GSGGNAGIAR FDSPDPEAEP DVVGGKGGDG GKGGSGLGVG GAGGTGGAGG NGGAGGLLFG    480
NGGNGGNAGA GGDGGAGVAG GVGGNGGGGG TATFHEDPVA GVWAVGGVGG DGGSGGSSLG    540
VGGVGGAGGV GGKGGASGML IGNGGNGGSG GVGGAGGVGG AGGDGGNGGS GGNASTFGDE    600
NSIGGAGGTG GNGGNGANGG NGGAGGIAGG AGGSGGFLSG AAGVSGADGI GGAGGAGGAG    660
GAGGSGGEAG AGGLTNGPGS PGVSGTEGMA GAPG                                694
<212> Type : PRT
<211> Length : 694
      SequenceName : SEQ ID 158
      SequenceDescription :

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<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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AYQALSAQAQ AFHAQFVQAL TSGGGAYAAA EAAATSPLLA PINEFFLANT GRPLIGNGTN    120
GAPGTGANGG DGGWLIGNGG AGGSGAAGVN GGAGGNGGAG GLIGNGGAGG AGGRASTGTG    180
GAGGAGGAAG MLFGAAGVGG PGGFAAAFGA TGGAGGAGGN GGLFADGGVG GAGGATDAGT    240
GGAGGSGGNG GLFGAGGTGG PGGFGIFGGG AGGDGGSGGL FGAGGTGGSG GTSIINVGGN    300
GGAGGDAGML SLGAAGGAGG SGGSNPDGGG GAGGIGGDGG TLFGSGGAGG VCGLGFDAGG    360
AGGAGGKAGL LIGAGGAGGA GGGSFAGAGG TGGAGGAPGL VGNAGNGGNG GASANGAGAA    420
GGAGGSGVLI GNGGNGGSGG TGAPAGTAGA GGLGGQLLGR DGFNAPASTP LHTLQQQILN    480
AINEPTQALT GRPLIGNGAN GTPGTGADGG AGGWLFGNGG NGGHGATGAD GGDGGSGGAG    540
GILSGIGGTG GSGGIGTTGQ GGTGGTGGAA LLIGSGGTGG SGGFGLDTGG AGGRGGDAGL    600
FLGAAGTGGQ AALSQNFIGA GGTAGAGGTG GLFANGGAGG AGGFGANGGT GGNGLLFGAG    660
GTGGAGTLGA DGGAGGHGGL FGAGGTGGAG GSSGGTFGGN GGSGGNAGLL ALGASGGAGG    720
SGGSALNVGG TGGVGGNGGS GGSLFGFGGA GGTGGSSGIG SSGGTGGDGG TAGVFGNGGD    780
GGAGGFGADT GGNSSSVPNA VLIGNGGNGG NGGKAGGTPG AGGTSGLIIG ENGLNGL       837

<212> Type : PRT
<211> Length : 837
      SequenceName : SEQ ID 159
      SequenceDescription :

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<213> OrganismName : Mycobacterium tuberculosis H37Rv
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AYQAASAEAA AFHGRFVQAL TTGGGAYAAA EAAAVTPLLN SINAPVLAAT GRPLIGNGAN    120
GAPGTGANGG DAGWLIGNGG AGGSGAKGAN GGAGGPGGAA GLFGNGGAGG AGGTATANNG    180
IGGAGGAGGS AMLFGAGGAG GAGGAATSLV GGIGGTGGTG GNAGMLAGAA GAGGAGGFSF    240
STAGGAGGAG GAGGLFTTGG VGGAGGQGHT GGAGGAGGAG GLFGAGGMGG AGGFGDHGTL    300
GTGGAGGDGG GGGLFGAGGD GGAGGSGLTT GGAAGNGGNA GTLSLGAAGG AGGTGGAGGT    360
VFGGGKGGAG GAGGNAGMLF GSGGGGGTGG FGFAAGGQGG VGGSAGMLSG SGGSGGAGGS    420
GGPAGTAAGG AGGAGGAPGL IGNGGNGGNG GESGGTGGVG GAGGNAVLIG NGGEGGIGAL    480
AGKSGFGGFG GLLLGADGYN APESTSPWHN LQQDILSFIN EPTEALTGRP LIGNGDSGTP    540
GTGDDGGAGG WLFGNGGNGG AGAAGTNGSA GGAGGAGGIL FGTGGAGGAG GVGTAGAGGA    600
GGAGGSAFLI GSGGTGGVGG AATTTGGVGG AGGNAGLLIG AAGLGGCGGG AFTAGVTTGG    660
AGGTGGAAGL FANGGAGGAG GTGSTAGGAG GAGGAGGLYA HGGTGGPGGN GGSTGAGGTG    720
GAGGPGGLYG AGGSGGAGGH GGMAGGGGGV GGNAGSLTLN ASGGAGGSGG SSLSGKAGAG    780
GAGGSAGLFY GSGGAGGNGG YSLNGTGGDG GTGGAGQITG LRSGFGGAGG AGGASDTGAG    840
GNGGAGGKAG LYGNGGDGGA GGDGATSGKG GAGGNAVVIG NGGNGGNAGK AGGTAGAGGA    900
GGLVLGRDGQ HGLT                                                      914
<212> Type : PRT
<211> Length : 914
      SequenceName : SEQ ID 160
      SequenceDescription :

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<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MSLVIVTPET VAAAASDVAR IGSSIGVANS AAAGSTTSVL AAGADEVSAA IATLFGSHAR     60
EYQAISTQVA AFHDRFAQTL SAAVGSYVSA EATNAAPLAT LEHNVLNALN APTQALLGRP    120
LIGDGAAGAP GTGQAGGAGG ILWGNGGAGG SGAPGQVGGA GGAAGLFGTG GAGGAGGAGA    180
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AGGAGGSGGW LLGNGGVGGA GGQSLLGGAT GGAGGNAGLF GVGGTGGPGG PGGPGGVGGT 240
GGAGGLGGTL YGAGGHGGAG GPGPIGGVGG HGGVGGAAGL LGVGGHGGAG GHGAEGVAGA 300
AGEDLSPHGT SGGVGGDAGD GGTGGRGGWL AGAGGAGGAG GVGGTGGAGG AGFSRALIVA 360
GDNGGDGGNG GMGGAGGAGG PGGAGGLISL LGGQGAGGAG GTGGAGGVGG DRGAGGPGNQ 420
AFNAGAGGAG GHGGDPGAGG AGGTGGAGSI TGAQGAIGAT PTSGGNGGAG GNGANATTAG 480
TNGANGGPGG HGGLVGNGGA GGNGANGAAG TNASDSGAVG GKGNSGGNGG QGGAGGDGGT 540
LAGNGGAGGT GGRGADGGLG GSGAEGANAT TAGERGQDGG KGGNGGVGGT GGNAVAPGAN 600
GGHGGNGGNP GFSGAGGLGG LSGDGVTRAA QGATPDFADT GGKGGNGGNG ANAVAPGGTG 660
ASGGAGGNAG AGGKGGENII GDGGGGNGGA GGKGGAGTLL GLTVFGDNGG AGVLGDSTDP 720
DGSGGAGGAG GAGGAGGDPT I 741
<212> Type : PRT
<211> Length : 741
SequenceName : SEQ ID 161
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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HYQSLNAQAA AFHHSFVQTL NAAGGAYSSA EAANASAQAL EQNLLAVINA PAQALFGRPL 120
IGNGANGTAA SPNGGDGGIL YGNGGNGFSQ TTAGVAGGAG GSAGLIGNGG NGGAGGAGAA 180
GGAGGAGGWL LGNGGAGGPG GPTDVPAGTG GAGGAGGDAP LIGWGGNGGP GGFAAFGNGG 240
AGGNGGASGS LFGVGGAGGV GGSSEDVGGT GGAGGAGRGL FLGLGGDGGA GGTSNNNGGD 300
GGAGGTAGGR LFSLGGDGGN GGAGTAIGSN AGDGGAGGDS SALIGYAQGG SGGLGGFGES 360
TGGDGGLGGA GAVLIGTGVG GFGGLGGGSN GTGGAGGAGG TGATLIGLGA GGGGGIGGFA 420
VNVGNGVGGL GGQGGQGAAL IGLGAGGAGG AGGATVVGLG GNGGDGGDGG GLFSIGVGGD 480
GGNAGNGAMP ANGGNGGNAG VIANGSFAPS FVGFGGNGGN GVNGGTGGSG GILFGANGAN 540
GPS 543
<212> Type : PRT
<211> Length : 543
SequenceName : SEQ ID 162
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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AYQTLGTQAA AFHERFIQAL STAAGAYGSA EAANASPLQQ ALNVINAPTQ TLLGRPLIGN 120
GTNGAPGTGQ AGGPGGLLYG NGGNGGSGGV GQAGGAGGSA GLIGIGGTGG AGGAGAVGGV 180
GGNGGWLYGN GGAGGLGGTG VAGVNGGMGA AGGAGGNAYL FGSGGAGGQG GMGAAGADGV 240
NPTPTGTADA GSTGTDQTLG GNAIGGNGGP GDAGDAMTSG GAGGSGGNAV STVNGDAVGG 300
EGGKGGEGAY GGAGGAGGSA ASIGNAAIGG NGGAGGNAQA PGGVGGAGGE GGDAQVGTNS 360
PSNAEAGNGG SGGNGFDSFA SGGTGGAGGT GGAGGRGGLL IGDGGAGGAG GVGGTGGSGA 420
PGGGGGAGGD GGAANTDSAG SSRKAFGGDG GVGGDGASAL GTGGEGGIGG QGGNGGAGGL 480
LIGNGGAGGV GGTAGAGGTG GSGGAGGAGG AGGGGTNSGP GAAFGGNGNT GGNGGNGGAP 540
GALGGKGGSG GLIGRAGSDG GVGAGGAGGA GGAGGTGGEG GTGGDGKTTD GNPGMGGSPG 600
SAGQPG 606
<212> Type : PRT
<211> Length : 606
SequenceName : SEQ ID 163
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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TYQALRTQAA AFHQQIVQTL TSTAGAYASA EAANVEQQLL GAINAPTMAL LGRPLIGHGA 120
DGAPGTGQAG GAGGILYGNG GNGGSGATGQ AGGAGGAAGL IGHGGAGGLG GTGASGGAGG 180
AGGWLWGNGG AGGNGGVGVA GDPGGVGGAG GAGGAAGLWG SGGSGGTGGQ GGVGGGKSGD 240
GGTGGIGGAG GGGGWLHGDG GAGGHGGQGG TGVSSGGNGG AGGTGGDGRG LSGSGGAGGR 300
GGQTGVGGKV GENNFGGAGG AGGTGGLIGN GGAGGNGGQG AISGAGGAGG NAWLIGDGGA 360
GGNGGDIRGQ GGGAGGAGGA GGQLIGNGGT GGAGGTVTSP NGLGGAGGAG GSAGLIGHGG 420
TGGAGGHSAQ GPDGNGGIGG AGGAGGNGGQ LYGTGGTGGT GGKGGDGFGV FGKGGAGGTG 480
GRGGAAGLIG DAGTGGTGGK GGTAGEDGTG GNGGTGGNGG AAVLIGNGGG GGAGGNGGAG 540

NDGTPGNGGG GGVGGTGGTL FGQPGQPGPP GQPGPA 576
<212> Type : PRT
<211> Length : 576
SequenceName : SEQ ID 164
SequenceDescription :

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<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MWTSQMIVAP AFVDAAAKDL ATIGSAISRA NAEALVPITA LLPAGADDVS AAIAALFATH 60
GQAYQELSAH AVAFHEQFVQ LMSAGAAQYA SAEAANSSPL QIVGQTALDA INSPVQTLTG 120
RPLIGNGANG VAGTGQNGGD GGWLYGNGGN GGSGGTGQNG GNGGSAGLWG SGGNGGQGGA 180
GANGAAGQPG KAGGSGGNGG AGGWIYGHGG HGGAGGNGGN ATAPGGASAG FDGGAGGNGG 240
SGGRGGLLFG NGGNGSVGGM GGQGTNDTAG DSAGSGGLGG NGGNGAQGGW LIGNGGQGGD 300
SGAGGGTDST QTGVMNGASG GSAGIAGNGG DAGLVGNGGA GGNGGNGAAG SALGTTIFGG 360
SGGVGGSGGD GGNGGWLFGS GASGGNGGQG GDAGTNGFAG FGGSAGGGGW VGAVNFGPIS 420
VQGFGLFGHG GDGGNGGDVG AGSLSIQFGA SGGDGGQGGV LYGNGGNGGN AGSGGGTGFE 480
GSAGQGGAAI LIGNGGAGGN GATGGTGVGN IIQEAGGDGS DGGAGGSGGL LFGSGGAGGI 540
GGAGGVGGSG NDGGNGGDGG QGGASGLGIG NGGPGGSGGT GGAGGTGGSA GTGGAGGDGG 600
NAALLIGTGG DGGDGVPPAP GGQGGKGGLI GLPGQNGQP 639
<212> Type : PRT
<211> Length : 639
SequenceName : SEQ ID 165
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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AYQAASAQAA AFYAQFVQAL SAGGGAYAAA EAAAVSPLLA PINAQFVAAT GRPLIGNGAN 120
GAPGTGANGG PGGWLIGNGG AGGSGAPGAG AGGNGGAGGL FGSGGAGGAS TDVAGGAGGA 180
GGAGGNAGML FGAAGVGGVG GFSNGGATGG AGGAGGAGGL FGAGRERGSG GSGNLTGGAG 240
GAGGNAGTLA TGDGGAGGTG GASRSGGFGG AGGAGGDAGM FFGSGGSGGA GGISKSVGDS 300
AAGGAGGAPG LIGNGGNGGN GGASTGGGDG GPGGAGGTGV LIGNGGNGGS GGTGATLGKA 360
GIGGTGGVLL GLDGFTAPAS TSPLHTLQQD VINMVNDPFQ TLTGRPLIGN GANGTPGTGA 420
DGGAGGWLFG NGGNGGQGTI GGVNGGAGGA GGAGGILFGT GGTGGSGGPG ATGLGGIGGA 480
GGAALLFGSG GAGGSGGAGA VGGNGGAGGN AGALLGAAGA GGAGGAGAVG GNGGAGGNGG 540
LFANGGAGGP GGFGSPAGAG GIGGAGGNGG LFGAGGTGGA GGGSTLAGGA GGAGGNGGLF 600
GAGGTGGAGS HSTAAGVSGG AGGAGGDAGL LSLGASGGAG GSGGSSLTAA GVVGGIGGAG 660
GLLFGSGGAG GSGGFSNSGN GGAGGAGGDA GLLVGSGGAG GAGASATGAA TGGDGGAGGK 720
SGAFGLGGDG GAGGATGLSG AFHIGGKGGV GGSAVLIGNG GNGGNGGNSG NAGKSGGAPG 780
PSGAGGAGGL LLGENGLNGL M 801
<212> Type : PRT
<211> Length : 801
SequenceName : SEQ ID 166
SequenceDescription :

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<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
GQSYQAVSAQ AAAFHDRFVQ LLNAGGGSYA SAEIANAQQN LLNAVNAPTQ TLLGRPLVGD 60
GADGASGPVG QPGGDGGILW GNGGNGGDST SPGVAGGAGG SAGLIGNGGR GGNGAPGGAG 120
GNGGLGGLLL GNGGAGGVGG TGDNGVGDLG AGGGGGDGGL GGRAGLIGHG GAGGNGGDGG 180
HGGSGKAGGS GGSGGFGQFG GAGGLLYGNG GAAGSGGNGG DAGTGVSSDG FAGLGGSGGR 240
GGDAGLIGVG GGGGGNGGDP GLGARLFQVG SRGGDGGVGG WLYGDGGGGG DGGNGGLPFI 300
GSTNAGNGGS ARLIGNGGAG GSGGSGAPGS VSSGGVGGAG NPGGSGGNGG VWYGNGGAGG 360
AAGQGGPGMN TTSPGGPGGV GGHGGTAILF GDGGAGGAGA AGGPGTPDGA AGPGGSGGTG 420
GLLFGVPGPS GPDG 434
<212> Type : PRT
<211> Length : 434
SequenceName : SEQ ID 167
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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PASAAMAAAA APYAGFLTTA SAQAQLAAGQ AKAVASVFEA AKAAIVPPAA VAANREAFLA 120
LIRSNWLGLN APWIAAVESL YEEYWAADVA AMTGYHAGAS QAAAQLPLPA GLQQFLNTLP 180
NLGIGNQGNA NLGGGNTGSG NIGNGNKGSS NLGGGNIGNN NIGSGNRGSD NFGAGNVGTG 240
NIGFGNQGPI DVNLLATPGQ NNVGLGNIGN NNMGFGNTGD ANTGGGNTGN GNIGGGNTGN 300
NNFGFGNTGN NNIGIGLTGN NQMGINLAGL LNSGSGNIGI GNSGTNNIGL FNSGSGNIGV 360
FNTGANTLVP GDLNNLGVGN SGNANIGFGN AGVLNTGFGN ASILNTGLGN AGELNTGFGN 420
AGFVNTGFDN SGNVNTGNGN SGNINTGSWN AGNVNTGFGI ITDSGLTNSG FGNTGTDVSG 480
FFNTPTGPLA VDVSGFFNTA SGGTVINGQT SGIGNIGVPG TLFGSVRSGL NTGLFNMGTA 540
ISGLFNLRQL LG 552
<212> Type : PRT
<211> Length : 552
SequenceName : SEQ ID 168
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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AYQALSAHVA AFHDQFVHTL TAGAGSYMAA EAAAASPLQA LQLELLNAIN APTLALLGRP 120
LIGDGTDAAP GSGGAGGAGG ILIGNGGTGG ASDLAGTGRG GVGGAGGAGG LFGIGGAGGG 180
CGSAVAIGGD GGAGGAGGVF SGGGAGGAGD AIGGSGGAGG TGGLLGGGGG AGGAGGAGGN 240
GGGASNSASI GGDGGSGGAG GMLYGAGGVG GNGGAAVAIG GDGGAGGRAG AIGNGGDGGN 300
GGTSNTPGGS GGDGGNGGNA GLIGNGGNGG NAEIVISGGS VAGTGGNGGL LLGFNGTNGL 360
P 361
<212> Type : PRT
<211> Length : 361
SequenceName : SEQ ID 169
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
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GVGPGSTGGA GGKGGAGANG GSSNGNARGG NAGNGGHGGA GGSGDTGGAG GAGGQGGFGG 120
TGGSGSGIGG GAGGNGGNGG AGGTGVVLGG KGGDGGNGDH GGPATNPGSG SRGGAGGSGG 180
NGGAGGNATG SGGKGGAGGN GGDGSFGATS GPASIGVTGA PGGNGGKGGA GGSNPNGSGG 240
DGGKGGNGGA GGNGGSIGAN SGIVGGSGGA GGAGGAGGNG SLSSGEGGKG GDGGHGGDGV 300
GGNSSVTQGG SGGGGGAGGA GGSGFFGGKG GFGGDGGQGG PNGGGTVGTV AGGGGNGGVG 360
GRGGDGVFAG AGGQGGLGGQ GGNGGGSTGG NGGLGGAGGG GGNAPDGGFG GNGGKGGQGG 420
IGGGTQSATG LGGDGGDGGD GGNGGNSGAK AGGAGGKGQA GQPNSGTEPG FGGDGGLGGA 480
GATP 484
<212> Type : PRT
<211> Length : 484
SequenceName : SEQ ID 170
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii
<400> PreSequenceString :
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GGREIKISAD KANAIIGGIN TLKELPDFGG VEVSQNVSIG PLNAGEDLNT NFGPLKFISN 120
NVTSIITGVG TKTFSNIDFA GKNATLQINK DLNITTKIDN TVAGNNGSIT FEGSGIISNH 180
IGYTNSLLGI NVGNGEAKIY APEANNITIN AKNINLTHNN SILTLCDGNI TTLKGNINNT 240
TEIDGQGILN LAYDLGSSSI ITGDIGNIGS LDTINVLLGS ATFNSTILKA TNINLKHNTS 300
TLNLDDNIIV IGNIKGNNNK DILNFKVHGT NLDNEMIIPA PQKTHGTLNF KGNATLNGNI 360
NNLNILKFSG GHGKTLNLQG NTKVDNLVFA DSVLDSGTIS VNGLLDTDCV TFNNSNVNGG 420
TLIINAKNTI SAKLLNATKA KIQINANLTM NHPSAGDISD IRIADNTIYT IDAKNGNVNL 480
LNNNAKIIFE GADSMLALIN TGVTADRTFT IYNNLNQSGN DEYGIVKIEA IKKVITIANQ 540
SGPYTIGQDN THRLKELIVE GAGDIIIDDT IFTKLLSINS TGQITFNRTL DLGAGGNIAF 600
GKHGTLVVNG VTGSITTSEN NQGILTINSG NITGVIGTNE LGLKLVNIGA DPVTCSANVF 660

ASVALTNPSS VLILADGVTL TGEVTTHNNT KGVLSLGTGS NITGQIGTNS AALEKINIGA 720
GASNIDSNIY AGSTVLTDQT SELTLNNDVV VNSNIITTAG NNSGKLIFTG NGGITGNIGA 780
NGAALQEVVF NGTTNIGGTA NSQNFTVAHS AANVVITGLT TGALKYKDTG TIIAHGGLVG 840
DIDFNNKAGK FILGDGAMID GSVLCNGGVA GTLDFIGDGN VTQNIGADNA NSISTINIQG 900
DNTKNVTIAN DIFVDNIHFT NGGILQLGGN LTTHNIDFGA NGGTLEFNGN NTYNLNAIIV 960
NGQNGILNAF TNLKASDDTI GTVKIINIGQ IGTPQNFTIQ VNNKNLTLVS SVNSSINFGD 1020
ANSQLILSAP VDQTIKFINN LNETGGGIIT LDSNGNNLTI SGNNGIKLGS KGNELSSLNI 1080
KGKVTVTNDL DIQNIHQLNI NNGALFDDQS LTSAKIKNIN IGTVAGGATY TLDAINDNFD 1140
LNTSGMVFKH QDSILELKNS SNTNDHTITL TSALDPGNNQ FGIIKLITDT NKLTIDNNGN 1200
VAYTLGTANH MLKQLTFASI DNGAIALKVG INVENVTLNI KDIELNEVNA NVLFNKNTTY 1260
TATGNINGHV DFQGNAGVIN LNDDIEIDGS VTSTGNVNGT LNFNGSGKVT GLINNIVMLQ 1320
AGAGDVSLSA SGNYSITEIQ GNGNNNLTFA ANSHLTTDIN KTGGQDLNLV FINGGSVSGS 1380
IGANAAVGDI IINAGSVNFS NTLKSGNIVI SDGATMQVNN NVTATDISGK NANNGTLKLN 1440
NHTPINITST LGNNNAIGTI EVANNDVTIT GTLQAQNIHF SNATQAATLT LGAASQVTNI 1500
TTAGNNIHTL EVTDFDTGND GIIGDANNRL KSIELTGNGT VTINSPHVYS SITTANNAQG 1560
NVKLNIEGGI TYDLGSKIKS LANVQISEDT TIRGDVYSKY LNIDAGKTIN FDRGDNNMNP 1620
KNLDIPDALI DLDVLPRSLS LFNYFTDIKA DNLNFADDTA TANFKDAVVI DAHIDNGGIL 1680
KFNDNAWLTQ EIKNANIIEI ASDKFMLLQK NIKAATLIAD NANLVLLDNV EVNTNLNVRD 1740
IVLDLANYEL KYTGNVTHNG LLTIITYFDT ALQKGGHILV SQGSNVDMSD LDNLIIKIKA 1800
HSDITNITSD TKHQIVKLET GAIYTPVPQT KVIIDASEEQ NKFVKWVADA NGLVLLTDTG 1860
GRDDTGGRDD TRGRGNTDNG CRDNCDVGNI SNNSSNEAGG SSSDKNYGIT DVVPIFDPSP 1920
ILDYTKNNYV ASGIANQLIN HVKDFGNTTD AGKLLNDLGF MSPNRVTETL DRLSNRINVN 1980
GLNEGVVGLN GIEVENFLTD IAINMDNFTA KEIGNRLEEL SDANTVNGLN KTNTLLNNKI 2040
NLKRLNTNNQ AIIAAGDEDN IVTGIWGMSF YGKIKQNSKN SASGYQSNTG GGIIGFDYNI 2100
DNSIVIGAAY TMADSKVKHK NDKNGDRTKA KSNIYSIYGL YNWLTNNFFV EAIGVYGRNK 2160
IKNYEKRITT ITDQIAIGKF INTFYSYELL GGYNYLISHR TTITPMFGMR YATFKNNGYK 2220
ENNTTFQNLS IKKNYYDKFE TILGLNSVTH YLSQDIIIKP ELHWFINYQC KNKLPNIDAR 2280
LDGIDEPLTT IRFKPAKITY NLGGGISTKN NMIEFGIRYN LSLAKKYTAH QGSLKIKVNL 2340

<212> Type : PRT
<211> Length : 2340
SequenceName : SEQ ID 171
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii
<400> PreSequenceString :
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ANIPVAPNSV ITANANNPIT FNTPNGHLNS LFLDTANDLA VTINEDTTLG FITNIAQQAK 120
FFNFTVAAGK ILNITGQGIT VQEASNTINA QNALTKVHGG AAINANDLSG LGSITFAAAP 180
SVLEFNLINP TTQEAPLTLG ANSKIVNGGN GTLNITNGFI QVSDNTFAGI KTINIDDCQG 240
LMFNSTPDAA NTLNLQVGGN TINFNGIDGT GKLVLVSKNG AATEFNVTGT LGGNLKGIIE 300
LNTAAVAGKL ISQGGAANAV IGTDNGAGRA AGFIVSVDNG NAATISGQVY AKNMVIQSAN 360
AGGQVTFEHI VDVGLGGTTN FKTADSKVII TENSNFGSTN FGNLDTQIVV PDTKILKGNF 420
IGDVKNNGNT AGVITFNANG ALVSASTDPN IAVTNINAIE AEGAGVVELS GIHIAELRLG 480
NGGSIFKLAD GTVINGPVNQ NALMNNNALA AGSIQLDGSA IITGDIGNGG VNAALQHITL 540
ANDASKILAL DGANIIGANV GGAIHFQANG GTIKLTNTQN NIVVNFDLDI TTDKTGVVDA 600
SSLTNNQTLT INGSIGTVVA NTKTLAQLNI GSSKTILNAG DVAINELVIE NNGSVQLNHN 660
TYLITKTINA ANQGQIIVAA DPLNTNTTLA DGTNLGSAEN PLSTIHFATK AANADSILNV 720
GKGVNLYANN ITTNDANVGS LHFRSGGTSI VSGTVGGQQG HKLNNLILDN GTTVKFLGDT 780
TFNGGTKIEG KSILQISNNY TTDHVESADN TGTLEFVNTD PITVTLNKQG AYFGVLKQVI 840
ISGPGNIVFN EIGNVGIVHG IAANSISFEN ASLGTSLFLP SGTPLDVLTI KSTVGNGTVD 900
NFNAPIVVVS GIDSMINNGQ IIGDKKNIIA LSLGSDNSIT VNANTLYSGI RTTKNNQGTV 960
TLSGGMPNNP GTIYGLGLEN GSPKLKQVTF TTDYNNLGSI IANNVTINDY VTLTTGGIAG 1020
TDFDAKITLG SVNGNANVRF VDSTFSDPRS MIVATQANKG TVTYLGNALV SNIGSLDTPV 1080
ASVRFTGNDS GAGLQGNIYS QNIDFGTYNL TILNSNVILG GGTTAINGEI DLLTNNLIFA 1140
NGTSTWGDNT SISTTLNVSS GNIGQVVIAE DAQVNATTTG TTTIKIQDNA NANFSGTQAY 1200
TLIQGGARFN GTLGAPNFAV TGSNIFVKYE LIRDSNQDYV LTRTNDVLNV VTTAVGNSAI 1260
ANAPGVSQNI SRCLESTNTA AYNNMLLAKD PSDVATFVGA IATDTSAAVT TVNLNDTQKT 1320
QDLLSNRLGT LRYLSNAETS DVAGSATGAV SSGDEAEVSY GVWAKPFYNI AEQDKKGGIA 1380
GYKAKTTGVV VGLDTLASDN LMIGAAIGIT KTDIKHQDYK KGDKTDINGL SFSLYGSQQL 1440
VKNFFAQGNA IFTLNKVKSK SQRYFFESNG KMSKQIAAGN YDNMTFGGNL IFGYDYNAMP 1500
NVLVTPMAGL SYLKSSNENY KETGTTVANK RINSKFSDRV DLIVGAKVAG STVNITDIVI 1560
YPEIHSFVVH KVNGKLSNSQ SMLDGQTAPF ISQPDRTAKT SYNIGLSANI KSDAKMEYGI 1620
GYDFNSASKY TAHQGTLKVR VNF 1643
<212> Type : PRT

<211> Length : 1643
SequenceName : SEQ ID 172
SequenceDescription :

Sequence

<213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :
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ADASFSPTNF VLDGTASADI PAGTYDYVII NPNPGIIYIV GEGVSKGNDY VVEAGKTYHF 120
TVQRQGPGDA ASVVVTGEGG NEFAPVQNLQ WSVSGQTVTL TWQAPASDKR TYVLNESFDT 180
QTLPNGWTMI DADGDGHNWL STINVYNTAT HTGDGAMFSK SWTASSGAKI DLSPDNYLVT 240
PKFTVPENGK LSYWVSSQEP WTNEHYGVFL STTGNEAANF TIKLLEETLG SGKPAPMNLV 300
KSEGVKAPAP YQERTIDLSA YAGQQVYLAF RHFGCTGIFR LYLDDVAVSG EGSSNDYTYT 360
VYRDNVVIAQ NLTATTFNQE NVAPGQYNYC VEVKYTAGVS PKVCKDVTVE GSNEFAPVQN 420
LTGSAVGQKV TLKWDAPNGT PNPNPGTTTL SESFENGIPA SWKTIDADGD GNNWTTTPPP 480
GGSSFAGHNS AICVSSASYI NFEGPQNPDN YLVTPELSLP NGGTLTFWVC AQDANYASEH 540
YAVYASSTGN DASNFANALL EEVLTAKTVV TAPEAIRGTR VQGTWYQKTV QLPAGTKYVA 600
FRHFGCTDFF WINLDDVEIK ANGKRADFTE TFESSTHGEA PAEWTTIDAD GDGQGWLCLS 660
SGQLGWLTAH GGTNVVASFS WNGMALNPDN YLISKDVTGA TKVKYYYAVN DGFPGDHYAV 720
MISKTGTNAG DFTVVFEETP NGINKGGARF GLSTEANGAK PQSVWIERTV DLPAGTKYVA 780
FRHYNCSDLN YILLDDIQFT MGGSPTPTDY TYTVYRDGTK IKEGLTETTF EEDGVATGNH 840
EYCVEVKYTA GVSPKECVNV TVDPVQFNPV QNLTGSAVGQ KVTLKWDAPN GTPNPNPGTT 900
TLSESFENGI PASWKTIDAD GDGNNWTTTP PPGGTSFAGH NSAICVSSAS YINFEGPQNP 960
DNYLVTPELS LPNGGTLTFW VCAQDANYAS EHYAVYASST GNDASNFANA LLEEVLTAKT 1020
VVTAPEAIRG TRVQGTWYQK TVQLPAGTKY VAFRHFGCTD FFWINLDDVE IKANGKRADF 1080
TETFESSTHG EAPAEWTTID ADGDGQGWLC LSSGQLDWLT AHGGTNVVAS FSWNGMALNP 1140
DNYLISKDVT GATKVKYYYA VNDGFPGDHY AVMISKTGTN AGDFTVVFEE TPNGINKGGA 1200
RFGLSTEANG AKPQSVWIER TVDLPAGTKY VAFRHYNCSD LNYILLDDIQ FTMGGSPTPT 1260
DYTYTVYRDG TKIKEGLTET TFEEDGVATG NHEYCVEVKY TAGVSPKECV NVTVDPVQFN 1320
PVQNLTGSAV GQKVTLKWDA PNGTPNPNPG TTTLSESFEN GIPASWKTID ADGDGNNWTT 1380
TPPPGGTSFA GHNSAICVSS ASYINFEGPQ NPDNYLVTPE LSLPNGGTLT FWVCAQDANY 1440
ASEHYAVYAS STGNDASNFA NALLEEVLTA KTVVTAPEAI RGTRVQGTWY QKTVQLPAGT 1500
KYVAFRHFGC TDFFWINLDD VEIKANGKRA DFTETFESST HGEAPAEWTT IDADGDGQGW 1560
LCLSSGQLGW LTAHGGTNVV ASFSWNGMAL NPDNYLISKD VTGATKVKYY YAVNDGFPGD 1620
HYAVMISKTG TNAGDFTVVF EETPNGINKG GARFGLSTEA NGAKPQSVWI ERTVDLPAGT 1680
KYVAFRHYNC SDLNYILLDD IQFTMGGSPT PTDYTYTVYR DGTKIKEGLT ETTFEEDGVA 1740
TGNHEYCVEV KYTAGVSPKE CVNVTINPTQ FNPVQNLTAE QAPNSMDAIL KWNAPASKRA 1800
EVLNEDFENG IPASWKTIDA DGDGNNWTTT PPPGGSSFAG HNSAICVSSA SYINFEGPQN 1860
PDNYLVTPEL SLPGGGTLTF WVCAQDANYA SEHYAVYASS TGNDASNFAN ALLEEVLTAK 1920
TVVTAPEAIR GTRVQGTWYQ KTVQLPAGTK YVAFRHFGCT DFFWINLDDV VITSGNAPSY 1980
TYTIYRNNTQ IASGVTETTY RDPDLATGFY TYGVKVVYPN GESAIETATL NITSLADVTA 2040
QKPYTLTVVG KTITVTCQGE AMIYDMNGRR LAAGRNTVVY TAQGGHYAVM VVVDGKSYVE 2100
KLAVK 2105
<212> Type : PRT
<211> Length : 2105
SequenceName : SEQ ID 173
SequenceDescription :

Sequence

<213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :
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EDSNGIKVNV KLADGVEYVV GTAVVSVTQG NAVTVAETNV SNPNEPVFTV KSADGNNVVE 120
LGTIVKLTIK RRAVCTAWSN AINAAETGFV FKDKVTVTIG DHSDSKESNS YSVNYPNLTI 180
KQPAPQVNKQ IGETIVREFS ITNGSQNPTQ TVYLSIEYPD EAYLTGVGAM TLQAKLGASG 240
TYADLTPTVT NGKVRIYTLS GSSLGPDHLL TNGEIIYLKE TFKLKTCAPV TVYRVGWGCS 300
IDSQCEIKTT AATITMAAGA ANITGYSVTG PDYRSPTFSL CQPFELTIKF SNSGAGGSMG 360
AAFNINTIGR NDYYRPRGFV LHEFIDVKVN GKPVTNFKTD GSELDLRFDG QFTEDPDGPG 420
VGLDDVDGDG FYDDLPVGAT ITITVTVRLK CDQFTACNNA PNDLSDRGLI LKTLYQTSCD 480
RTSWIDPNTW FNLSSTHLYL SRESVQDASH MPTVIEKDTP FDLKIMTSYY SILSSYNNIW 540
YANPNTRYVV EIVFPQGMTM PPKSDIEWTN IKNHPIDGSL VFTPPINLPD ANITTSGNTM 600
TIVSPSQERG FVTLHGVKYD CTNNHEMVVE YKIREVFNYL HFPDCLCPVG PIMCNTAKRY 660
VLGCDPPCGR GAETSVPKIE RADNSLGWTD YTMRTRQSRS NISAYDLAKA LYMDEVNITA 720
TSIQHGTASS LGARFVLATG VDRVETLTPL SADIKIFRDG VQIVSVDGYT TFRSIRRNNN 780
AEQVIDWDFT SILPAGGLLD RDKVDVVTRY RVTSQNAHRV DTQVGREWFF YNSTANVSPI 840

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WDEANPLTCL ILVPEIYIMG TFVVNGTDPH VISQCTPTDL GRVANHYARR FGSGAFEYAN    900
EYRPGVKIRN IYLKVPKSYT LNRVEYSNHR NHSSLGTTMP FEEINHTDVT SQGEYNIYKY    960
QLADNEKAHF NITVKNAYGA ALKVNVSPTC ASSAVATNYD KISYYVDYID YYYYAATQPT   1020
VPNSLDIVAD QSAGSNGIYS VSALNVYNRP ILYTNKPSIA LVNQSGEVEL VGKTGEWKLR   1080
ISNPSSATAP YVWLALPTTS GLTIEKVTDA AGTEMAFTTY SGGKMYRLSE AGVPVGSALD   1140
YTIHFTYSGC SPIALKAMGG WNCSAYPLSL DEYVCSSQVI DLKLKPLPAA MELTEIAVPD   1200
PTAAATLCST LEYIYSIQST DNANVYSPTF SIFPEEGLVV TPNQVQVEYP AGSGNWAALN   1260
VVNNSVNLLQ HPALTTIGYL KGLKEGESND NQRKILVKFY IKTECSFVSG KNFRVRADGR   1320
NACNQNAKGS GLAISTPPIR INGAIEPYTT SASTQLVTTT TSQSDCKAPK RVKVVQTVVG   1380
GETTPKAYLE ITLPLGFKYV TGSYAPDNTH PGGVNASPAG TEEVTLTANG EDKIKINVKA   1440
GLTSGQSFAY TLEMKEDDDN VPACGNHTIE IVNVEEIEGL WCEGVQCAET LVVTGANKFE   1500
FELDKPYLDI TVISAVSTFS GGKENLTIEY KVSNTSTTQP LKPGAVVTLF SDKDNNQVFS   1560
GGDVAVATQE LVAEITNTTP LTQIMKVKGV SSSHTGNLVL TILPKDGCYC EIKSPMVTLN   1620
HLPSNYWIGG TVGKPNEWKE PNNWTNDQVP DAAEDVEFAT EVNNPTDPNN PKSGPAKENL   1580
HLDDIHQNGT AGRVIGNLIN DSDKDLVITT GNQLTINGVV EDNNPNVGTI VVKSSKDNPT   1740
GTLLFANPGN NQNVGGTVEF YNQGYDCADC GMYRRSWQYF GIPVNESDFP YDHVDGNATV   1800
NQWVEPFNGD KWRPAPYAPD TKLQKFKGYQ ITNDVQAQPT GVYSFKGTLC VCDAFLNLTR   1860
TSGVNYSGAN LIGNSYTGAI DIKQGIVFPP EVEQTVYLFN TGTRDQWRKL NGSTVSGYRA   1920
GQYLSVPKNT AGQDNLPDRI PSMHSFLVKM QNGASCTLQI LYDKLLKNTT VNNGNGTQIT   1980
WRSGNSGSAN MPSLVMDVLG NESADRLWIF TDGGLSFGFD NGWDGRKLTE KGLSQLYAMS   2040
DIGNDKFQVA GVPELNNLLI GFDADKDGQY TLEFALSDHF AKGGVFLEDL SRGVTRRVVD   2100
GGSYSFDAKR GDSGARFRLS YDEEWVESAE VSVLVGTAGK RIVITNNSEH ACQANVYTTD   2160
GKLLIRLDVK PGSKSMTEPL VDGVYVVSLQ SPATSSNVRK VVVN                    2204
<212> Type : PRT
<211> Length : 2204
      SequenceName : SEQ ID 174
      SequenceDescription :

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<213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :
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NPEDLIAQSR WQSQRDGRPV RIGQVIPVDV DFASKASHIS SIGDVDVYRL QFKLEGAKAI    120
TLYYDAFNIP EGGRLYIYTP DHEIVLGAYT NATHRRNGAF ATEPVPGSEL IMDYEVSRGG    180
TLPDIKISGA GYIFDKVGGR PVTDNHYGIG EDDSDSDCEI NINCPEGADW QAEKNGVVQM    240
IMVKGQYISM CSGNLLNNTK GDFTPLIISA GHCASITTNF GVTQSELDKW IFTFHYEKRG    300
CSNGTLAIFR GNSIIGASMK AFLPIKGKSD GLLLQLNDEV PLRYRVYYNG WDSTPDIPSS    360
GAGIHHPAGD AMKISILKKT PALNTWISSS GSGGTDDHFY FKYDQGGTEG GSSGSSLFNQ    420
NKHVVGTLTG GAGNCGGTEF YGRLNSHWNE YASDGNTSRM DIYLDPQNNG QTTILNGTYR    480
DGYKPLPSVP RLLLQSTGDQ VELNWTAVPA DQYPSSYQVE YHIFRNGKEI ATTKELSYSD    540
AIDESIIGSG IIRYEVSARF IYPSPLDGVE SYKDTDKTSA DLAIGDIQTK LKPDVTPLPG    600
GGVSLSWKVP FLSQLVSRFG ESPNPVFKTF EVPYVSAAAA QTPNPPVGVV IADKFMAGTY    660
PEKAAIAAVY VMPSAPDSTF HLFLKSNTNR RLQKVTTPSD WQAGTWLRIN LDKPFPVNND    720
HMLFAGIRMP NKYKLNRAIR YVRNPDNLFS ITGKKISYNN GVSFEGYGIP SLLGYMAIKY    780
LVVNTDAPKI DMSLVQEPYA KGTNVAPFPE LVGIYVYKNG TFIGTQDPSV TTYSVSDGTE    840
SDEYEIKLVY KGSGISNGVA QIENNNAVVA YPSVVTDRFS IKNAHMVHAA ALYSLDGKQV    900
RSWNNLRNGV TFSVQGLTAG TYMLVMQTAN GPVSQKIVKQ                         940
<212> Type : PRT
<211> Length : 940
      SequenceName : SEQ ID 175
      SequenceDescription :

Sequence
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<213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :
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KGMIMRNEDP KKIPYVYGKS YSQNKFFPGE IATLDDPFIL RDVRGQVVNF APLQYNPVTK    180
TLRIYTEITV AVSETSEQGK NILNKKGTFA GFEDTYKRMF MNYEPGRYTP VEEKQNGRMI    240
VIVAKKYEGD IKDFVDWKNQ RGLRTEVKVA EDIASPVTAN AIQQFVKQEY EKEGNDLTYV    300
LLIGDHKDIP AKITPGIKSD QVYGQIVGND HYNEVFIGRF SCESKEDLKT QIDRTIHYER    360
NITTEDKWLG QALCIASAEG GPSADNGESD IQHENVIANL LTQYGYTKII KCYDPGVTPK    420
NIIDAFNGGI SLANYTGHGS ETAWGTSHFG TTHVKQLTNS NQLPFIFDVA CVNGDFLFSM    480
PCFAEALMRA QKDGKPTGTV AIIASTINQS WASPMRGQDE MNEILCEKHP NNIKRTFGGV    540
TMNGMFAMVE KYKKDGEKML DTWTVFGDPS LLVRTLVPTK MQVTAPAQIN LTDASVNVSC    600
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DYNGAIATIS ANGKMFGSAV VENGTATINL TGLTNESTLT LTVVGYNKET VIKTINTNGE 660
PNPYQPVSNL TATTQGQKVT LKWDAPSTKT NATTNTARSV DGIRELVLLS VSDAPELLRS 720
GQAEIVLEAH DVWNDGSGYQ ILLDADHDQY GQVIPSDTHT LWPNCSVPAN LFAPFEYTVP 780
ENADPSCSPT NMIMDGTASV NIPAGTYDFA IAAPQANAKI WIAGQGPTKE DDYVFEAGKK 840
YHFLMKKMGS GDGTELTISE GGGSDYTYTV YRDGTKIKEG LTATTFEEDG VAAGNHEYCV 900
EVKYTAGVSP KVCKDVTVEG SNEFAPVQNL TGSAVGQKVT LKWDAPNGTP NPNPNPNPNP 960
NPGTTTLSES FENGIPASWK TIDADGDGHG WKPGNAPGIA GYNSNGCVYS ESFGLGGIGV 1020
LTPDNYLITP ALDLPNGGKL TFWVCAQDAN YASEHYAVYA SSTGNDASNF TNALLEETIT 1080
AKGVRSPEAI RGRIQGTWRQ KTVDLPAGTK YVAFRHFQST DMFYIDLDEV EIKANGKRAD 1140
FTETFESSTH GEAPAEWTTI DADGDGQGWL CLSSGQLDWL TAHGGTNVVS SFSWNGMALN 1200
PDNYLISKDV TGATKVKYYY AVNDGFPGDH YAVMISKTGT NAGDFTVVFE ETPNGINKGG 1260
ARFGLSTEAD GAKPQSVWIE RTVDLPAGTK YVAFRHYNCS DLNYILLDDI QFTMGGSPTP 1320
TDYTYTVYRD GTKIKEGLTE TTFEEDGVAT GNHEYCVEVK YTAGVSPKKC VNVTVNSTQF 1380
NPVKNLKAQP DGGDVVLKWE APSAKKTEGS REVKRIGDGL FVTIEPANDV RANEAKVVLA 1440
ADNVWGDNTG YQFLLDADHN TFGSVIPATG PLFTGTASSD LYSANFEYLI PANADPVVTT 1500
QNIIVTGQGE VVIPGGVYDY CITNPEPASG KMWIAGDGGN QPARYDDFTF EAGKKYTFTM 1560
RRAGMGDGTD MEVEDDSPAS YTYTVYRDGT KIKEGLTETT YRDAGMSAQS HEYCVEVKYT 1620
AGVSPKVCVD YIPDGVADVT AQKPYTLTVV GKTITVTCQG EAMIYDMNGR RLAAGRNTVV 1680
YTAQGGYYAV MVVVDGKSYV EKLAIK 1706

<212> Type : PRT
<211> Length : 1706
SequenceName : SEQ ID 176
SequenceDescription :

Sequence

<213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :
MKRKPLFSAL VILSGFFGSV HPASAQKVPA PVDGERIIME LSEADVECTI KIEAEDGYAN 60
DIWADLNGNG KYDSGERLDS GEFRDVEFRQ TKAIVYGKMA KFLFRGSSAG DYGATFIDIS 120
NCTGLTAFDC FANLLTELDL SKANGLTFVN CGKNQLTKLD LPANADIETL NCSKNKITSL 180
NLSTYTKLKE LYVGDNGLTA LDLSANTLLE ELVYSNNEVT TINLSANTNL KSLYCINNKM 240
TGLDVAANKE LKILHCNNNQ LTALNLSANT KLTTLSFFNN ELTNIDLSDN TALEWLFCNG 300
NKLTKLDVSA NANLIALQCS NNQLTALDLS KTPKLTTLNC YSNRIKDTAM RALIESLPTI 360
TEGEGRFVPY NDDEGGEEEN VCTTEHVEMA KAKNWKVLTS WGEPFPGITA LISIEGESEY 420
SVYAQDGILY LSGMEQGLPV QVYTVGGSMM YSSVASGSAM EIQLPRGAAY VVRIGSHAIK 480
TAMP 484

<212> Type : PRT
<211> Length : 484
SequenceName : SEQ ID 177
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKRAITLFAV LLMGWSVNAW SFACKTANGT AIPIGGGSAN VYVNLAPVVN VGQNLVVDLS 60
TQIFCHNDYP ETITDYVTLQ RGSAYGGVLS NFSGTVKYSG SSYPFPTTSE TPRVVYNSRT 120
DKPWPVALYL TPVSSAGGVA IKAGSLIAVL ILRQTNNYNS DDFQFVWNIY ANNDVVVPTG 180
GCDVSARDVT VTLPDYPGSV PIPLTVYCAK SQNLGYYLSG TTADAGNSIF TNTASFSPAQ 240
GVGVQLTRNG TIIPANNTVS LGAVGTSAVS LGLTANYART GGQVTAGNVQ SIIGVTFVYQ 300

<212> Type : PRT
<211> Length : 300
SequenceName : SEQ ID 178
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MGIKQHNGNT KADRLAELKI RSPSIQLIKF GAIGLNAIIF SPLLIAADTG SQYGTNITIN 60
DGDRITGDTA DPSGNLYGVM TPAGNTPGNI NLGNDVTVNV NDASGYAKGI IIQGKNSSLT 120
ANRLTVDVVG QTSAIGINLI GDYTHADLGT GSTIKSNDDG IIIGHSSTLT ATQFTIENSN 180
GIGLTINDYG TSVDLGSGSK IKTDGSTGVY IGGLNGNNAN GAARFTATDL TIDVQGYSAM 240
GINVQKNSVV DLGTNSTIKT NGDNAHGLWS FGQVSANALT VDVTGAAANG VEVRGGTTTI 300
GADSHISSAQ GGGLVTSSSD ATINFSGTAA QRNSIFSGGS YGASAQTATA VINMQNTDIT 360

VDRNGSLALG LWALSGGRIT GDSLAITGAA GARGIYAMTN SQIDLTSDLV IDMSTPDQMA 420
IATQHDDGYA ASRINASGRM LINGSVLSKG GLINLDMHPG SVWTGSSLSD NVNGGKLDVA 480
MNNSVWNVTS NSNLDTLALS HSTVDFASHG STAGTFTTLN VENLSGNSTF IMRADVVGEG 540
NGVNNRGDLL NISGSSAGNH VLAIRNQGSE ATTGNEVLTV VKTTDGAASF SASSQVELGG 600
YLYDVRKNGT NWELYASGTV PEPTPNPEPT PAPAQPPIVN PDPTPEPAPT PKPTTTADAG 660
GNYLNVGYLL NYVENRTLMQ RMGDLRNQSK DGNIWLRSYG GSLDSFASGK LSGFDMGYSG 720
IQFGGDKRLS DVMPLYVGLY IDSTHASPDY SGGDGTARSD YMGMYASYMA QNGFYSDLVI 780
KASRQKNSFH VLDSQNNGVN ANGTANGMSI SLEAGQRFNL SPTGYGFYIE PQTQLTYSHQ 840
NEMAMKASNG LNIHLNHYES LLGRASMILG YDITAGNSQL NVYVKTGAIR EFSGDTEYLL 900
NDSREKYSFK GNGWNNGVGV SAQYNKQHTF YLEADYTQGN LFDQKQVNGG YRFSF 955

<212> Type : PRT
<211> Length : 955
SequenceName : SEQ ID 179
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MSKFVKTAIA AAMVMGVFTS TATIAAGNNG TARFYGTIED SVCSIVPDDH KLEVDMGDIG 60
AEKLKNNGTT TPKSFQIRLQ DCVFDTQETM TTTFTGTVSS ANSGNYYTIF NTDTGAAFNN 120
VSLAIGDSLG TSYKSGMGID QKIVKDTSTN KGKAKQTLNF NAWLVGAADA PDLGNFEANT 180
TFQITYL 187
<212> Type : PRT
<211> Length : 187
SequenceName : SEQ ID 180
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKIKTLAIVV LSALSLSSAA ALADTTTVNG GTIHFKGEVV NAACAVDAGS VDQTVQLGQV 60
RTASLKQAGA TSSAVGFNIQ LNDCDTTVAT KAAVAFLGTA IDATRTDVLA LQSSAAGSAT 120
NVGVQILDRT GNALTLDGAT FSAQTTLNNG TNTIPFQARY YAIGEATPGA ANADATFKVQ 180
YQ 182
<212> Type : PRT
<211> Length : 182
SequenceName : SEQ ID 181
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MASISSLGVG SGLDLSSILD SLTAAQKATL TPISNQQSSF TAKLSAYGTL KSALTTFQTA 60
NTALSKADLF SATSTTSSTT AFSATTAGNA IAGKYTISVT HLAQAQTLTT RTTRDDTKTA 120
IATSDSKLTI QQGDDKDPIT IDISAANSSL SGIRDAINNA KAGVSASIIN VGNGEYRLSV 180
TSNDTGLDNA MTLSVSGDDA LQSFMGYDAS ASSNGMEVSV AAQNAQLTVN NVAIENSSNT 240
ISDALENITL NLNDVTTGNQ TLTITQDTSK VQTAIKDWVN AYNSLIDTFS SLTKYTAVDA 300
GADSQSSSNG ALLGDSTLRT IQTQLKSMLS NTVSSSSYKT LAQIGITTDP SDGKLELDAD 360
KLTAALKKDA SGVGALIVGD GKKTGITTTI GSNLTSWLST TGIIKAATDG VSKTLNKLTK 420
DYNAASDRID AQVARYKEQF TQLDVLMTSL NSTSSYLTQQ FENNSNSK 468
<212> Type : PRT
<211> Length : 468
SequenceName : SEQ ID 182
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MEGKADNVVL ENGGRLDVLT GHTATNTRVD DGGTLDVRNG GTATTVSMGN GGVLLADSGA 60
AVSGTRSDGK AFSIGGGQAD ALMLEKGSSF TLNAGDTATD TTVNGGLFTA RGGTLAGTTT 120
LNNGAILTLS GKTVNNDTLT IREGDALLQG GALTGNGSVE KSGSGTLTVS NTTLTQKAVN 180
LNEGTLTLND STVTTDVIAQ RGTALKLTGS TVLNGAIDPT NVTLASGATW NIPDNATVQS 240

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VVDDLSHAGQ IHFTSTRTGK FVPATLKVKN LNGQNGTISL RVRPDMAQNN ADRLVIDGGR    300
ATGKTILNLV NAGNSASGLA TSGKGIQVVE AINGATTEEG AFIQGNKLQA GAFNYSLNRD    360
SDESWYLRSE NAYRAEVPLY ASMLTQAMDY DRILAGSRSH QTGVSGENNS VRLSIQGGHL    420
GHDNNGGIAR GATPESSGSY GFVRLEGDLL RTEVAGMSVT AGVYGAAGHS SVDVKDDDGS    480
RAGTVRDDAG SLGGYLNLIH NASGLWADIV AQGTRHSMKA SSDNNDFRVR GWGWLGSLET    540
GLPFSITDNL MLEPQLQYTW QGLSLDDGQD NASYVKFGHG SAQHVRAGFR LGSHHDMNFG    600
KGTSSRDTLR GSAKHSVREL PVNWWVQPSV IRTFSSRGDM SMGTAAAGSN MTFSPSQNGT    660
SLDLQAGLEA RVRENITLGV QASYAHSING SSAEGYNSQA TLNVTF                   706
<212> Type : PRT
<211> Length : 706
      SequenceName : SEQ ID 183
      SequenceDescription :

Sequence
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<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MAFSQAVSGL NAAATNLDVI GNNIANSATY GFKSGTASFA DMFAGSKVGL GVKVAGITQD     60
FTDGTTTNTG RGLDVAISQN GFFRLVDSNG SVFYSRNGQF KLDENRNLLN TQGLQLTGYP    120
VTGTPPTIQQ GANPTNISIP NTLMAAKTTT TASMQINLNS SDPLPTVTPF SASNADSYNK    180
KGSVTVFDSQ GNAHDMSVYF VKTGDNNWQV YTQDSSDPNS IAKTATTLEF NANGTLVDGA    240
MANNIATGAI NGAEPATFSL SFLNSMQQNT GANNIVATTQ NGYKPGDLVS YQINDDGTVV    300
GNNSNEQTQL LGQIVLANFA NNEGLASEGD NVWSATQSSG VALLGTAGTG NFGTLTNGAL    360
EASNVDLSKE LVNMIVAQRN YKSNAQTIKT QDQILNTRVN LR                       402
<212> Type : PRT
<211> Length : 402
      SequenceName : SEQ ID 184
      SequenceDescription :

Sequence
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<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKLVHMASGL AVAIALAACA DKSADIQTPA PAANTSISAT QQPAIQQPNV SGTVWIRQKV     60
ALPPDAVLTV TLSDASLADA PSKVLAQKAV RTEGKQSPFS FVLPFNPADV QPNARILLSA    120
AITVNDKLVF ITDTVQPVIN QGGTKADLTL VPVQQTAVPV QASGGATTTV PSTSPTQVNP    180
SSAVPAPTQY                                                           190
<212> Type : PRT
<211> Length : 190
      SequenceName : SEQ ID 185
      SequenceDescription :

Sequence
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<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MIIKKSGGRW QLSLLASVVI SAFFLNTAYA WQQEYIVDTQ PGHSTERYTW DSDHQPDYND     60
ILSQRIQSSQ RALGLEVNLA EETPVDVTSS MSMGWNFPLY EQVTTGPVAA LHYDGTTTSM    120
YNEFGDSTTT LTDPLWHASV SSLGWRVDSR LGDLRPWAQI SYNQQFGENI WKAQSGLSRM    180
TATNQNGNWL DVTVGADMLL NQNIAAYAAL TQAENTTNNS DYLYTMGVSA RF            232

<212> Type : PRT
<211> Length : 232
      SequenceName : SEQ ID 186
      SequenceDescription :

Sequence
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<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKWCKRGYVL AAMLALASAT IQAADVTITV NGKVVAKPCT VSTTNATVDL GDLYSFSLMS     60
AGAASAWHDV ALELTNCPVG TSRVTASFSG AADSTGYYKN QGTAQNIQLE LQDDSGNTLN    120
TGATKTVQVD DSSQSAHFPL QVRALTVNGG ATQGTIQAVI SITYTYS                  167
<212> Type : PRT
<211> Length : 167
      SequenceName : SEQ ID 187
      SequenceDescription :
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Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKRAPLITGL LLISTSCAYA SSGGCGADST SGATNYSSVV DDVTVNQTDN VTGREFTSAT 60
LSSTNWQYAC SCSAGKAVKL VYMVSPVLTT TGHQTGYYKL NDSLDIKTTL QANDIPGLTT 120
DQVVSVNTRF TQIKSSTVYS AATQTGVCQG DTSRYGPVNI GANTTFTLYV TKPFLGSMTI 180
PKTDIAVIKG AWVDGMGSPS TGDFHDLVKL SIQGNLTAPQ SCKINQGDVI KVNFGFINGQ 240
KFTTRNAMPD GFTPVDFDIT YDCGDTSKIK NSLQMRIDGT TGVVDQYNLV ARRRSSDNVP 300
DVGIRIENLG GGVANIPFQN GILPVDPSGH GTVNMRAWPV NLVGGELETG KFQGTATITV 360
MVR 363
<212> Type : PRT
<211> Length : 363
SequenceName : SEQ ID 188
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MQKNAAHTYA ISSLLVLSLT GCAWIPSTPL VQGATSAQPV PGPTPVANGS IFQSAQPINY 60
GYQPLFEDRR PRNIGDTLTI VLQENVSASK SSSANASRDG KTNFGFDTVP RYLQGLFGNA 120
RADVEASGGN TFNGKGGANA SNTFSGTLTV TVDQVLVNGN LHVVGEKQIA INQGTEFIRF 180
SGVVNPRTIS GSNTVPSTQV ADARIEYVGN GYINEAQNMG WLQRFFLNLS PM 232

<212> Type : PRT
<211> Length : 232
SequenceName : SEQ ID 189
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKRHLNTCYR LVWNHITGAF VVASELARAQ GKRGGVAVAL SLAAVTSLPV LAADIVVHPG 60
ETVNGGTLVN HDNQFVSGTA DGVTVSTGLE LGPDSDENTG GQWIKAGGTG RNTTVTANGR 120
QIVQAGGTAS DTVIRDGGGQ SLNGLAVNTT LDNRGEQWVH GGGKAAGTII NQDGYQTIKH 180
GGLATGTIVN TGAEGGPESE NVSSGQMVGG TAESTTINKN GRQVIWSSGM ARDTLIYAGG 240
DQTVHGEAHN TRLEGGNQYV HNGGTATETL INRDGWQVIK EGGTAAHTTI NQKESCR 297

<212> Type : PRT
<211> Length : 297
SequenceName : SEQ ID 190
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MMMKTIKHLL CCAIAASALI STGVHAASWK DALSSAASEL GNQNSTTQEG GWSLASLTNL 60
LSSGNQALSA DNMNNAAGIL QYCAKQKLAS VTDAENIKNQ VLEKLGLNSE EQKEDTNYLD 120
GIQGLLKTKD GQQLNLDNIG TTPLAEKVKT KACDLVLKQG LNFIS 165
<212> Type : PRT
<211> Length : 165
SequenceName : SEQ ID 191
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MFKGQKTLAA LAVSLLFTAP VYAADEGSGE IHFKGEVIEA PCEIHQDDID KEVELGQVTT 60
SHINQSHHSD AVAVDLLLVN CDLENSSNGS GGKISKVAVT FDSSAKTTGA DPILNNTSTG 120
EATGVGVRLM NKDQSNIVLG TATPDIDLAP TSSEQTLNFF AWMEQIDQAT PVTPGAVTAN 180
ATYVLDYK 188
<212> Type : PRT

<211> Length : 188
SequenceName : SEQ ID 192
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MSAGSPKFTV RRIAALSLVS LWLAGCSDTS NPPAPVSSVN GNAPANTNSG MLITPPPKMG 60
TTSTAQQPQI QPVQQPQIQA TQQPQIQPVQ PVAQQPVQME NGRIVYNRQY GNIPKGSYSG 120
STYTVKKGDT LFYIAWITGN DFRDLAQRNN IQAPYALNVG QTLQVGNASG TPITGGNAIT 180
QADAAEQGVV IKPAQNSTVA VASQPTITYS ESSGEQSANK MLPNNKPTAT TVTAPVTVPT 240
ASTTEPTVSS TSTSTPISTW RWPTEGKVIE TFGASEGGNK GIDIAGSKGQ AIIATADGRV 300
VYAGNALRGY GNLIIIKHND DYLSAYAHND TMLVREQQEV KAGQKIATMG STGTSSTRLH 360
FEIRYKGKSV NPLRYLPQR 379
<212> Type : PRT
<211> Length : 379
SequenceName : SEQ ID 193
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MIKFLSALIL LLVTTAAQAE RIRDLTSVQG VRQNSLIGYG LVVGLDGTGD QTTQTPFTTQ 60
TLNNMLSQLG ITVPTGTNMQ LKNVAAVMVT ASLPPFGRQG QTIDVVVSSM GNAKSLRGGT 120
LLMTPLKGVD SQVYALAQGN ILVGGAGASA GGSSVQVNQL NGGRITNGAV IERELPSQFG 180
VGNTLNLQLN DEDFSMAQQI ADTINRVRGY GSATALDART IQVRVPSGNS SQVRFLADIQ 240
NMQVNVTPQD AKVVINSRTG SVVMNREVTL DSCAVAQGNL SVTVNRQANV SQPDTPFGGG 300
QTVVTPQTQI DLRQSGGSLQ SVRSSASLNN VVRALNALGA TPMDLMSILQ SMQSAGCLRA 360
KLEII 365
<212> Type : PRT
<211> Length : 365
SequenceName : SEQ ID 194
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKRSIIAAAV FSSFFMSAGV FAADVDTGTL TIKGNIAESP CKFEAGGDSV SINMPTVPTT 60
VFEGKAKYST YDDAVGVTSS MLKISCPKEV AGVKLSLITN DKITGNDKAI ASSNDTVGDN 120
SDVLDVSAPF NIESYKTAEG QYAIPFKAKY LKLTDNSVQS GDVLSSLVMR VAQD 174

<212> Type : PRT
<211> Length : 174
SequenceName : SEQ ID 195
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MAVQKNVIKG ILAGTFALML SGCVTVPDAI KGSSTTPQQD LVRVMSAPQL YVGQEARFGG 60
KVVAVQNQQG KTRLEIATVP LDSGARPTLG EPSRGRIYAD VNGFLDPVDF RGQLVTVVGP 120
ITGAVDGKIG NTPYKFMVMQ VTGYKRWHLT QQVIMPPQPI DPWFYGGRGW PYGYGGWGWY 180
NPGPARVQTV VTE 193
<212> Type : PRT
<211> Length : 193
SequenceName : SEQ ID 196
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MRNKPFYLLC AFLWLAVSRV LAADSTITIR GYVRDNGCSV AAESTNFTVD LMENAAKQFN 60

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NIGATTPVVP FRILLSPCGN AVSAVKVGFT GVADSHNANL LALENTVSAA AGLGIQLLNE      120
QQNQIPLNAP SSAISWTTLT PGKPNTLNFY ARLMATQVPV TAGHINATAT FTLEYQ          176

<212> Type : PRT
<211> Length : 176
      SequenceName : SEQ ID 197
      SequenceDescription :

Sequence
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<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKKLTVAALA VTTLLSGSAF AHEAGEFFMR AGSATVRPTE GAGGTLGSLG GFSVTNNTQL       60
GLTFTYMATD NIGVELLAAT PFRHKIGTRA TGDIATVHHL PPTLMAQWYF GDASSKFRPY      120
VGAGINYTTF FDNGFNDHGK EAGLSDLSLK DSWGAAGQVG VDYLINRDWL VNMSVWYMDI      180
DTTANYKLGG AQQHDSVRLD PWVFMFSAGY RF                                    212
<212> Type : PRT
<211> Length : 212
      SequenceName : SEQ ID 198
      SequenceDescription :

Sequence
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<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MFFKRGKILS AGRLNKKSLG IVMFLSVGLL LAGCSGSKSS DTGTYSGSVY TVKRGDTLYR       60
ISRTTGTSVK ELARLNGISP PYTIEVGQKL KLGGAKSSSS TRKSTAKSTT KTASVTPSSA      120
VPKSSWPPVG QRCWLWPTTG KVIMPYSTAD GGNKGIDISA PRGTPIYAAG AGKVVYVGNQ      180
LRGYGNLIMI KHSEDYITAY AHNDTMLVNN GQSVKAGQKI ATMGSTDAAS VRLHFQIRYR      240
ATAIDPLRYL PPQGSKPKC                                                   259
<212> Type : PRT
<211> Length : 259
      SequenceName : SEQ ID 199
      SequenceDescription :

Sequence
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<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MAQVINTNSL SLITQNNINK NQSALSSSIE RLSSGLRINS AKDDAAGQAI ANRFTSNIKG       60
LTQAARNAND GISVAQTTEG ALSEINNNLQ RIRELTVQAS TGTNSDSDLD SIQDEIKSRL      120
DEIDRVSGQT QFNGVNVLAK DGSMKIQVGA NDGQTITIDL KKIDSDTLGL NGFNVNGGGA      180
VANTAASKAD LVAANATVVG NKYTVSAGYD AAKASDLLAG VSDGDTVQAT INNGFGTAAS      240
ATNYKYDSAS KSYSFDTTTA SAADVQKYLT PGVGDTAKGT ITIDGSAQDV QISSDGKITA      300
SNGDKLYIDT TGRLTKNGSG ASLTEASLST LAANNTKATT IDIGGTSISF TGNSTTPDTI      360
TYSVTGAKVD QAAFDKAVST SGNNVDFTTA GYSVNGTTGA VTKGVDSVYV DNNEALTTSD      420
TVDFYLQDDG SVTNGSGKAV YKDADGKLTT DAETKAATTA DPLKALDEAI SSIDKFRSSL      480
GAVQNRLDSA VTNLNNTTTN LSEAQSRIQD ADYATEVSNM SKAQIIQQAG NSVLAKANQV      540
PQQVLSLLQG                                                             550
<212> Type : PRT
<211> Length : 550
      SequenceName : SEQ ID 200
      SequenceDescription :

Sequence
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<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKKIACLSAL AAVLAFTAGT SVAATSTVTG GYAQSDAQGQ MNKMGGFNLK YRYEEDNSPL       60
GVIGSFTYTE KSRTASSGDY NKNQYYGITA GPAYRINDWA SIYGVVGVGY GKFQTTEYPT      120
YKHDTSDYGF SYGAGLQFNP MENVALDFSY EQSRIRSVDV GTWIAGVGYR F               171

<212> Type : PRT
<211> Length : 171
      SequenceName : SEQ ID 201
      SequenceDescription :
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Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKRNIIGGAF TLASLMLAGH ALAEDGVVNF VGEIVDTTCE VTSDTADQIV PLGKVSKNAF 60
SGVGSLASPQ KFSIKLENCP ATYTQAAVRF DGTEAPGGDG DLKVGTPLTA GNPGDFTGTG 120
QAIAATGVGI RIFNQSDNSQ VKLYNDSAYT AIDAEGKAEM KFIARYVATN ATVTAGTANA 180
DSQFTVEYKK 190
<212> Type : PRT
<211> Length : 190
SequenceName : SEQ ID 202
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKKSTLALVV MGIVASASVQ AAEIYNKDGN KLDVYGKVKA MHYMSDNASK DGDQSYIRFG 60
FKGETQINDQ LTGYGRWEAE FAGNKAESDT AQQKTRLAFA GLKYKDLGSF DYGRNLGALY 120
DVEAWTDMFP EFGGDSSAQT DNFMTKRASG LATYRNTDFF GVIDGLNLTL QYQGKNENRD 180
VKKQNGDGFG TSLTYDFGGS DFAISGAYTN SDRTNEQNLQ SRGTGKRAEA WATGLKYDAN 240
NIYLATFYSE TRKMTPITGG FANKTQNFEA VAQYQFDFGL RPSLGYVLSK GKDIEGIGDE 300
DLVNYIDVGA TYYFNKNMSA FVDYKINQLD SDNKLNINND DTVAVGMTYQ F 351

<212> Type : PRT
<211> Length : 351
SequenceName : SEQ ID 203
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MRKQWLGICI AAGMLAACTS DDGQQQTVSV PQPAVCNGPI VEISGADPRF EPLNATANQD 60
YQRDGKSYKI VQDPSRFSQA GLAAIYDAEP GSNLTASGEA FDPTKLTAAH PTLPIPSYAR 120
ITNLANGRMI VVRINDRGPY GNDRVISLSR AAADRLNTSN NTKVRIDPII VAQDGSLSGP 180
GMACTTVAKQ TYALPAPPDL SGGAGTSSVS GPQGDILPVS NSTLKSEDPT GAPVTSSGFL 240
GAPTTLAPGV LEGSEPTPAP QPVVTASSTT PATSPAMVTP QAASQSASGN FMVQVGAVSD 300
QARAQQYQQQ LGQKFGVPGR VTQNGAVWRI QLGPFASKAE ASTLQQRLQT EAQLQSFITT 360
AQ 362
<212> Type : PRT
<211> Length : 362
SequenceName : SEQ ID 204
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKKKTIYQCV ILFFSLLNIH VGMAGPEQVS MHIYGNVVDQ GCDVATKSAL QNIHIGDFNI 60
SDFQAANTVS TAADLNIDIT GCAAGITGAD VLFSGEADTL APTLLKLTDT GGSGGMATGI 120
AVQILDAQSQ QEIPLNQVQP LTPLKAGDNT LKYQLRYKST KAGATGGNAT AVLYFDLVYQ 180

<212> Type : PRT
<211> Length : 180
SequenceName : SEQ ID 205
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKNKLLFMML TILGAPGIAA AAGYDLANSE YNFAVNELSK SSFNQAAIIG QAGTNNSAQL 60
RQGGSKLLAV VAQEGSSNRA KIDQTGDYNL AYIDQAGSAN DASISQGAYG NTAMIIQKGS 120
GNKANITQYG TQKTAVVVQR QSQMAIRVTQ R 151
<212> Type : PRT
<211> Length : 151

SequenceName : SEQ ID 206
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MMKFKKCLLP VAMLASFTLA GCQSNADDHA ADVYQTDQLN TKQETKTVNI ISILPAKVAV 60
DNSQNKRNAQ AFGALIGAVA GGVIGHNVGS GSNSGTTAGA VGGGAVGAAA GSMVNDKTLV 120
EGVSLTYKEG TKVYTSTQEG KECQFTTGLA VVITTTYNET RIQPNTKCPE KS 172

<212> Type : PRT
<211> Length : 172
SequenceName : SEQ ID 207
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MQTKKNEIWV GIFLLAALLA ALFVCLKAAN VTSIRTESTY TLYATFDNIG GLKARSPVSI 60
GGVVVGRVAD ITLDPKTYLP RVTLEIEQRY NHIPDTSSLS IRTSGLLGEQ YLALNVGFED 120
PELGTAILKD GDTIQDTKSA MVLEDLIGQF LYGSKGDDNK NSGDAPAAAP GNNETTEPVG 180
TTK 183
<212> Type : PRT
<211> Length : 183
SequenceName : SEQ ID 208
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MAPLAFSAQS LAESLTVEQR LELLEKALRE TQSELKKYKD EEKKKYTPAT VNRSVSTNDQ 60
GYAANPFPTS SAAKPDAVLV KNEEKNASET GSIYSSMTLK DFSKFVKDEI GFSYNGYYRS 120
GWGTASHGSP KSWAIGSLGR FGNEYSGWFD LQLKQRVYNE NGKRVDAVVM IDGNVGQQYS 180
TGWFGDNAGG ENFMQFSDMY VTTKGFLPFA PEADFWVGKH GAPKIEIQML DWKTQRTDAA 240
AGVGLENWKV GPGKIDIALV REDVDDYDRS LQNKQQINTH TIDLRYKDIP LWDKATLMVS 300
GRYVTANESA SEKDNQDNNG YYDWKDTWMF GTSLTQKFDK GGFNEFSFLV ANNSIARNFG 360
RYAGASPFTT FNGRYYGDHT GGTAVRLTSQ GEAYIGDHFI VANAIVYSFG NNIYSYETGA 420
HSDFESIRAV VRPAYIWDQY NQTGVELGYF TQQNKDANSN KFNESGYKTT LFHTFKVNTS 480
MLTSRLEIRF YATYIKALEN ELDGFTFEDN KDAQFAVGAQ AEIWW 525
<212> Type : PRT
<211> Length : 525
SequenceName : SEQ ID 209
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKRILSAVL VSGVTLSSAT TLSAVKADDF DAQIASQDSK INNLTAQQQA AQAQVNTIQG 60
QVSALQTQQA ELQAENQRLE AQSATLGQQI QTLSSKIVAR NESLKQQARS AQKSNAATSY 120
INAIINSKSV SDAINRVSAI REVVSANEKM LQQQEQDKAA VEQKQQENQA AINTVAANQE 180
TIAQNTNALN TQQAQLEAAQ LNLQAELTTA QDQKATLVAQ KAAAEEAARQ AAAAQAAAEA 240
KAAAEAKALQ EQAAQAQAAA NNNTQATDVS DQQAAAADNT QAAQTGDSTE QSAAQAVNNS 300
DQESTTATEA QPSASSASTA AVAANTSSAN TYPAGQCTWG VKSLAPWVGN YWGNGGQWAA 360
SAAAAGYRVG STPSAGAVAV WNDGGYGHVA YVTGVQGGQI QVQEANYAGN QSIGNYRGWF 420
NPGSVSYIYP N 431
<212> Type : PRT
<211> Length : 431
SequenceName : SEQ ID 210
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159

<400> PreSequenceString :
MKVKKTYGFR KSKISKTLCG AVLGTVAAVS VAGQKVFADE TTTTSDVDTK VVGTQTGNPA 60
TNLPEAQGSA SKEAEQSQNQ AGETNGSIPV EVPKTDLDQA AKDAKSAGVN VVQDADVNKG 120
TVKTAEEAVQ KETEIKEDYT KQAEDIKKTT DQYKSDVAAH EAEVAKIKAK NQATKEQYEK 180
DMAAHKAEVE RINAANAASK TAYEAKLAQY QADLAAVQKT NAANQAAYQK ALAAYQAELK 240
RVQEANAAAK AAYDTAVAAN NAKNTEIAAA NEEIRKRNAT AKAEYETKLA QYQAELKRVQ 300
EANAANEADY QAKLTAYQTE LARVQKANAD AKAAYEAAVA ANNAKNAALT AENTAIKQRN 360
ENAKATYEAA LKQYEADLAA VKKANAANEA DYQAKLTAYQ TELARVQKAN ADAKAAYEAA 420
VAANNAANAA LTAENTAIKK RNADAKADYE AKLAKYQADL AKYQKDLADY PVKLKAYEDE 480
QASIKAALAE LEKHKNEDGN LTEPSAQNLV YDLEPNANLS LTTDGKFLKA SAVDDAFSKS 540
TSKAKYDQKI LQLDDLDITN LEQSNDVASS MELYGNFGDK AGWSTTVSNN SQVKWGSVLL 600
ERGQSATATY TNLQNSYYNG KKISKIVYKY TVDPKSKFQG QKVWLGIFTD PTLGVFASAY 660
TGQVEKNTSI FIKNEFTFYD EDGKPINFDN ALLSVASLNR ENNSIEMAKD YTGKFVKISG 720
SSIGEKNGMI YATDTLNFRQ GQGGARWTMY TRASEPGSGW DSSDAPNSWY GAGAIRMSGP 780
NNSVTLGAIS STLVVPADPT MAIETGKKPN IWYSLNGKIR AVNVPKVTKE KPTPPVKPTA 840
PTKPTYETEK PLKPAPVAPN YEKEPTPPTR TPDQAEPNKP TPPTYETEKP LEPAPVEPSY 900
EAEPTPPTRT PDQAEPNKPT PPTYETEKPL EPAPVEPSYE AEPTPPTPTP DQPEPNKPVE 960
PTYEVIPTPP TDPVYQDLPT PPSVPTVHFH YFKLAVQPQV NKEIRNNNDI NIDRTLVAKQ 1020
SVVKFQLKTA DLPAGRDETT SFVLVDPLPS GYQFNPEATK AASPGFDVTY DNATNTVTFK 1080
ATAATLATFN ADLTKSVATI YPTVVGQVLN DGATYKNNFT LTVNDAYGIK SNVVRVTTPG 1140
KPNDPDNPNN NYIKPTKVNK NENGVVIDGK TVLAGSTNYY ELTWDLDQYK NDRSSADTIQ 1200
KGFYYVDDYP EEALELRQDL VKITDANGNE VTGVSVDNYT NLEAAPQEIR DVLSKAGIRP 1260
KGAFQIFRAD NPREFYDTYV KTGIDLKIVS PMVVKKQMGQ TGGSYENQAY QIDFGNGYAS 1320
NIIINNVPKI NPKKDVTLTL DPADTNNVDG QTIPLNTVFN YRLIGGIIPA DHSEELFEYN 1380
FYDDYDQTGD HYTGQYKVFA KVDITFKDGS IIKSGAELTQ YTTAEVDTAK GAITIKFKEA 1440
FLRSVSIDSA FQAESYIQMK RIAVGTFENT YINTVNGVTY SSNTVKTTTP EDPTDPTDPQ 1500
DPSSPRTSTV INYKPQSTAY QPSSVQETLP NTGVTNNAYM PLLGIIGLVT SFSLLGLKAK 1560
KD 1562
<212> Type : PRT
<211> Length : 1562
SequenceName : SEQ ID 211
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MLTELKAVLK KPMLWITMVG VALVPALYNI IFLSSMWDPY GKVSDLPVAV VNKDKTATYE 60
GKKMTIGKDM TDNMVRNKSL DYHFVDSEKA QKGLEKGDYY MIITLPEDLS QNAASVLTDE 120
PKKLTIPYQT SKGHSFVASK MSETAAKTLK ESVSKNITSS YTKSLFKNMS TLKTGLGSAA 180
NASQKIATGS KQLANGSQVM TDNLNLLSNS SQSFAQGTNT LYSGLTAYTG GVGQLSAGLN 240
NLNNGLTAYT NGVGQLANGS SQLSNQSQKL LGGVAQLANG SASIQQLVNA SSQLNQGLIK 300
LSTATGLSEE QVQQFSSLIN QLGTLNQSIQ NYSDNGTATT ANSPDLSTYL SAITTAAQAI 360
VNSGNTSQQT TTNQSNALAA VQATGAYQRL SAEDQSEIAA ALANTGSSTT TTGADANAVS 420
QAQAILNNVQ SIQSALSTLQ TTTANTPTSP SASLTQIKNT ANSVLPSAAT SLTTLSSGLT 480
QAKTALDSQV VPVSTALANG TAQLGSTFST GANSLMTGVG QYTNAVDILN AGANTLAAKN 540
NQLTDGTSQL VNGANQLNSN SGQLTKGTAQ LANGANQIET GAGKLAAGGE SLTAGLTTLS 600
SGSGELSKAL STAKNKLSLV AVDNDNAKTL SSPVTIKHTD KDNVKTNGVG MAPYMMSAAL 660
MVMAISTNTI FRVALSGKQA KTLREWIDQK LAVNGLIAVT GAIILYFGVH IIGLSANFEL 720
KTLGLIILTS ITFMVLVTTL VTWHDKFGSF AALILLLLQL GSSAGTYPLA VTDKFFQVVN 780
PYLPMSYSVS GLRETISMAG TIGNQLLALS LFFLTFAALG LLIARRRIRS VKVA 834

<212> Type : PRT
<211> Length : 834
SequenceName : SEQ ID 212
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MVSQKNKSKK GQSKTFTLIS NRINLLFFLI VALFTVLLLR LAQMQLYDAK FYKSKLTEST 60
TYTIKTSSPR GQIYDAKGVA LVENEVKEVV AFTRSNTMTA KDIKANAKKL ADMVTLTESK 120
VTKRQKKDYY LADPKNYQKI VKKLPNNKKY DNFGNNLTES KIYANAVKAV PNSAIDYSED 180
EKKIIHIFSQ MNATSVFNTA SLTTGDLTAE QIAVLATSKS DLKGISVKTD WERKTDKNSI 240
TSIIGKVSSQ KTGLPAEEAN NYVKKGYSLN DRVGTSYLEK QYENDLQGSR TVQAIKVNKE 300
GKIISDKTTA KGTKGKNLKL TLDLEFQKGV EQILNQYFNS ELASGNTKYS EGVYAVVLNP 360

NTGAVLSMAG LEHDLKTGEV SSNALGAVTE VFTPGSVVKG ATLTAGWENG VLSGNQVLND 420
QPIQFAGSSP INSWFTNGST PLTASQSLEY SSNTYMVQLA LKLMGQDYHS GMTLSTDGYK 480
EAMEKLRATY AQYGLGVSTG IDLPGESKGY TPEHYDPSNV LTESFGQFDN YTAMQLAQYA 540
AAVANGGKRI APHLVEGIYD NNKTGGLGNL VQSIDTKVLN NVSISSDDMG IIKEGFYNVV 600
NGGSYATGKT LAKGASVPIS AKTGTAEAYV TGDDGKSVYT SNLNVVAYAP SSNPQIAVAV 660
VLPHETDLHG TTSHAITRDI INLYQKMYPM NQ 692
<212> Type : PRT
<211> Length : 692
SequenceName : SEQ ID 213
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MTVLKYGLGI LLSAIILAII IGGLLFTYYV SSTPKLSEAK LKATNSSLVY DSNNNLIADL 60
GAEKRESISS DSIPMKLVNA VTSIEDHRFF KHRGVDIYRI IGAAWSNLLH KSTQGGSTLD 120
QQLIKLAYFS TKESDQTLKR KAQEVWLSLQ MEKKYTKEEI LTFYVNKVYM GNGNYGMRTA 180
AKSYYGKDLK DLSIAQLATL AGIPQAPTQY DPYAQPKAAT SRRNTVLSQM YKHKKITKRE 240
YDAAVATPIS DGLQELKRSS SYPKYMDNYL KQVISEVKKR TGQDIFSAGM KVYTNVNADA 300
QQYLWNIYNT DEYIAYPDDN FQVASTVMDV TNGKVIAQLG GRHQDTNVSF GTNQAVLTDR 360
DWGSTMKPIS AYGPALESEA FTTTAQMLND SVYYYPGTTT QVYDWDHRYN GWMTIQTAIQ 420
QSRNVPAVRA IDAAGLDTAK GFLSGLGIDY PEMRYSNAIS SNTSSSEQKY GASSEKMAAA 480
YAAFSNGGTY YEPQYVNKIE FKDGTSETYD AKGNRAMKET TAYMMTDMLK TVLTYGTGTE 540
AAIPGLYQAG KTGTSNYDDN ELVEMSEKLG INPYGLGTIA PDENFVGYTP QYSMAVWTGY 600
KNRLMPVYGD SMKIAAQVYR TMMAYLSSSG NSDWTMPDGL YRSGGYLYLN GSSGSNSRYG 660
AAPATSSSSS SSSSSDSNNN DQNNNQTTEA SSDSSSSSSD ATTSSNP 707
<212> Type : PRT
<211> Length : 707
SequenceName : SEQ ID 214
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKSKTAKITL LSSLALAAFG ATNVFADEAS TQLNSDTVAA PTADTQASEP AATEKEQSPV 60
VAVVESHTQG NTTTTTSQVT SKELEDAKAN ANQEGLEVTE TEAQKQPSVE AADADNKAQA 120
QTINTAVADY QKAKAEFPQK QEQYNKDFEK YQSDVKEYEA QKAAYEQYKK EVAQGLASGR 180
VEKAQGLVFI NEPEAKLSIE GVNQYLTKEA RQKHATEDIL QQYNTDNYTA SDFTQANPYD 240
PKEDTWFKMK VGDQISVTYD NIVNSKYNDK KISKVKINYT LNSSTNNEGS ALVNLFHDPT 300
KTIFIGAQTS NAGRNDKISV TMQIIFYDEN GNEIDLSGNN AIMSLSSLNH WTTKYGDHVE 360
KVNLGDNEFV KIPGSSVDLH GNEIYSAKDN QYKANGATFN GDGADGWDAV NADGTPRAAT 420
AYYGAGAMTY KGEPFTFTVG GNDQNLPTTI WFATNSAVAV PKDPGAKPTP PEKPELKKPT 480
VTWHKNLVVE TKTEEVPPVT PPTTPDEPTP EKPKTPEDPQ SPVVAKSVSF RTARKGEMRV 540
RERDYQPTLP HAGAAKQNGL ATLGAISTAF AAATLIAARK KEN 583
<212> Type : PRT
<211> Length : 583
SequenceName : SEQ ID 215
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MEQKIFSKRK SKIAGLCGAI LTTTVVALAS GTVIEADETI EQPVAAETVS QADGDNPEQT 60
TSVQQETAPQ QTKTSQSSDA TVDSEESATS PSDEQTVSQN DSNSSSQIDQ TIADTNRSDS 120
DHISKTSAAT TEDQEEKVNS AKAQTAAATN NQDTRYSAKD AYGNSNFNKT LTEFGKNANV 180
ADVTYNGVRD EYIVVNDPSA PYVPNANEIA KYLKEYLTEL RNINNIAIPV PSVDQVMQKY 240
AQDRANEEAN EKNGLDHDTN LPIPNNLTWV AEDGHLDMDS SIQSKSQEGY TLASDKATAY 300
YLALNWFSDY FNIYDDPNDG LKSFGHAVSI LSDGGTGMGL GLASGQDNEK GMWYAQLEFG 360
GNDNEDNTND FSSLKNGKGE WVLYYKGSPV KFLPNTTFWY VKKGTSPDAA STPHNSDKPS 420
FQSSKDLDPN FKADNRFQEG KEASVHQAIP ATFKSHRDEV GNKDQNSLSA QLPDTGVQKN 480
NQLALIALGT GLILLSGLLL SKRKSLK 507
<212> Type : PRT
<211> Length : 507
SequenceName : SEQ ID 216

SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MTFEKQKHFS LRKLKFGLVS VAIIAFLFAV TKTAEADETV ITEQRQTSKI NASSQKVENQ 60
TSNQVEAKTD SANKDPQEKT GSVATDAPSM NSANNMSQSD KQNTVNEISS DSQQTKTDEQ 120
TDLPQNSFKQ QSAHVKMTTE AEKTPSHSIN TFVNDGNGNW YYLGADGRNV TGSHTIGGKT 180
MYFAQDGKQV KGAFAQDSDG NKHYYDRDSG EMWTNRFVND QGNWYYLNND GVPVTGSITV 240
NGQSLYFNSD GSQVKGNFVE EDGSLRYYDK NSGDLLRKTS RTINGVNYQF DNDGNARAID 300
KIEVVKTSLV VDSYEFGPSV SKIILEFNHK VTPAVVHAGA MVTTAGVQRK ILNSYVSNAS 360
GHVVYFDSSH YVTLELDIPY DPNDSSRNAS PFIFDSAAFR NNWVNSYTVK VDNLQVQADG 420
SNSSQIISSE QDAINNRFLP TTDRFSERGS YGNFNYAAYQ PEAAIGGEKN PLIVWLHGIG 480
EVGTDINIPL LASNVARLTE DPIQSHFTST GSGGQKGAYV LVPQSSIPWS QNQTASLMAL 540
IKAYVASHPD IDSRRIYLAG VSNGGGMTLD MGVAYPNYFA ALVPIAASYS NQLTDNQITA 600
AALKALKGQP MWLIHTRTDK TISADSSVLP FYKELLQAGA QNKWLSYYET NVGKHHSGVT 660
YNGHWSWIYF LNDQVTGTQN TDNAKNWSGL SGMVATNPTY GGDAKATVNG RTYSNVFDWL 720
NGQRRR 726
<212> Type : PRT
<211> Length : 726
SequenceName : SEQ ID 217
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKIFIKKHQQ SILYYSLSFL LPSFIMFLVL FSKNIYWGSS TTILASDGFH QYVIFDALFR 60
NILHGTDSLF YSFKAGLGFN IFALTSYYLG SFLTPFTYFF NVKNMADAFY LFTLIKFGLI 120
GLSAFYSLGQ IYTKISKSLV LMLSTSYALM SFTSSQLELN NWLDVFILLP LIMLGLQRLV 180
EKRGIFLYFL TLTCLFIQNY YFGFMTAIFL TLWFFTQVSW DIRNRMKRLS DFVLVSIFAT 240
LTSAFMLLPT FLDLKSHGEV LTEQISLFSS DIWYFDFFAK SLLGSYDTTK YGSIPTIYIG 300
LLPLIFAITF FFVKSIKWQV KVAYFLLLAI IIASFIFQPL DLFWQGMHSP NMFLHRYSWA 360
FSLVIVIMAA ETLTRIKDIK LKNFYPAFTF LGVGLLATFL FKDYYNYLTQ VNFILTTIFL 420
VSYFIILFTF FNQLVSYKVI ISFTLIFTSF EIALNTFYQI EGIQTDWNFP SREVYEDNVK 480
EIDNYVKKTK KDNLEFFRTE KQIPQTYNDG MKFNYNSISQ FSSVKNNLSA QLLNSLGYYS 540
QGNHSTISYP NNTILMDSLF SIKYNINNQN PHKFGFHLKQ KNNKLQLYKN FYSLPLALMS 600
NHIYKDVKFD SYPLDNQQKF VNELTDLNLT LFKEIPIISS VGMQVLDNRV TINGSKGNKA 660
QVYYTVKCPA NSQLYISLPN LTVNNKDENV FITTNKHTSS YIIDESYYLF NLGNYKKTQT 720
LIFKLSFPKN KTVSYDLPHI YALDLTAYQK SIKQLKSQTV KTTTKKNKIF TTYVAKKRTS 780
LIYTLPYDKG WFAKQNGKAI KISKAQNGLM KIDVSKGSGK IIMTFVPQGL YQGILLTCLG 840
IFLFVFYQLY YKKFNLK 857
<212> Type : PRT
<211> Length : 857
SequenceName : SEQ ID 218
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKLKHILRIG AVAFASILLL TACGSKTSKK TVTLATVGTT NPFSYEKKGK LTGYDIEVAK 60
EVFKASDKYD VKYQKTEWTS IFSGLDSDKY QIGANNISYT KERANKYLYS NPTASNPLVL 120
VVPKDSDIKS YNDIAGHSTQ VVQGNTTVSM LQKFNKNHEN NQVKLNFTSE DLAHQIRNVS 180
DGKYDFKIFE KISAETIIKE QGLDNLKVID LPSDQKPYVY FIFAQDQKDL QKFVNKRLKK 240
LYENGTLEKL SKKYLGGSYL PDKKDMK 267
<212> Type : PRT
<211> Length : 267
SequenceName : SEQ ID 219
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MRFLVFLIAF FAAFYKFIET ERIDSNTVAV NPDSLILKRF LKTNQLNGIM IVTGPDGKAQ 60

VFSNQSKVDG SPVSIKDYFP LASLQKLITG VAIQQLIDKG KLSLNTPLSK YYPQIENSEN 120
ITIQNLLTHT SGLADRKEVP QQVLTTQEQQ LDFSLTNYRV TYRKKWKYAN INYALLAGII 180
SQISGQNYAT YVRQHFLTAG KGWHFKKYIQ IKDKSKLAAL SVMDQSTTWD KLSKEVTSTF 240
GAGDYASRPV DYWKFMMAFI NDQFVPVSEY QRSMKMTSKS YYGGLYISQK MLHANGGGFD 300
TYSCFAYSNP KTKQVMVLFI TNGKYKRVKS LAAKAFKLYA DSYALRKNET SK 352

<212> Type : PRT
<211> Length : 352
SequenceName : SEQ ID 220
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKKIALAAL SFVSAAVLAA CSSAPGGSSD AAGNKIGDTV KIGYNLELSG DVAAYGQAEK 60
NGANLAVEEI NKAGGIDGKK IKVISKDNKS DNGEASTIST NLATQSKVNA ILGPATSGAT 120
AAAAPNANDA AVPLVTPSGT QDNLTYSKGK VQDYIFRTTF QDSFQGKIIA KYATDNLKAK 180
KVALYYDKSS DYAQGIADAF KKAYKGKITV EDTFQAKDQD FQAALTKFKN KDFDAIVIPG 240
YYTETGLITK QARDMGLTQP ILGPDGFNDE KYVEGAGAAN TNNVHYVSGY STKVALTNKA 300
EKFLKDYKAK YGEEPNMFAA LAYDSVYMIA DAAKDAKTSK DIATNLAKLK NFKGVTGKMT 360
IDKKHNPVKS AVMVGLKDGK EDTATAVEAK 390
<212> Type : PRT
<211> Length : 390
SequenceName : SEQ ID 221
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKLSLLLLV CLSLLGLFAC TSKKTADKKL TVVATNSIIA DITKNIAGNK VVLHSIVPVG 60
RDPHEYEPLP EDVKKTSQAD VIFYNGINLE NGGNAWFTKL VKNAHKKTDK DYFAVSDSVK 120
TIYLENAKEK GKEDPHAWLD LKNGIIYAKN IMKRLSEKDP KNKSYYQKNF QAYSAKLEKL 180
HKVAKEKISR IPTEKKMIVT SEGCFKYFSK AYDIPSAYIW EINTEEEGTP NQIKALVKKL 240
RKSRVSALFV ESSVDDRPMK TVSKDTGIPI AAKIFTDSVA KKGQAGDSYY AMMKWNIDKI 300
ANGLSQ 306
<212> Type : PRT
<211> Length : 306
SequenceName : SEQ ID 222
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MFVHTKTKKK RKWQRKVFLL LLLFLLPIVS VLAFIVLFIG GGTAESHDVE ATTGGVKLSA 60
KQFADKTKLG ISEEEAKNAL AFADRLMSRH HFTAQATAGV LAVGFRESGF DVKAVNNSGG 120
VAGFFQWSGW GSSVNGDRWK VASKRELTLE VEVDLMSTEL DGRYADVVKK VGSATDEKQA 180
AKDWSQYYEG VAVSDGQTKA DKIESWATTI CEALKSGGTN YAKVNNTGTS STAIPQGWEN 240
ISAFDGHAYE GSENYPQGQC TWYVYNRAKQ LGVSFSPYMG NGGQWYQVQG YHSSHTPKAH 300
TALSFVNGQA GSDPTYGHVA FVEAVKDDGS ILISEMNVYG QPAMTVAYRT FDAETAKQFW 360
YVEGK 365
<212> Type : PRT
<211> Length : 365
SequenceName : SEQ ID 223
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKMKRKLLSL VSVLTILLGA FWVTKIVKAD QVTNYTNTAS ITKSDGTALS NDPSKAVNYW 60
EPLSFSNSIT FPDEVSIKAG DTLTIKLPEQ LQFTTALTFD VMHTNGQLAG KATTDPNTGE 120
VTVTFTDIFE KLPNDKAMTL NFNAQLNHNN ISIPGVVNFN YNNVAYSSYV KDKDITPISP 180
DVNKVGYQDK SNPGLIHWKV LINNKQGAID NLTLTDVVGE DQEIVKDSLV AARLQYIAGD 240
DVDSLDEAAS RPYAEDFSKN VTYQTNDLGL TTGFTYTIPG SSNNAIFISY TTRLTSSQSA 300

GKDVSNTIAI SGNNINYSNQ TGYARIESAY GRASSRVKRQ AETTTVTETT TSSSSETTTS 360
EATTETSSTT NNNSTTTETA TSTTGASTTQ TKTTASQTNV PTTTNITTTS KQVTKQKAKF 420
VLPSTGEQAG LLLTTVGLVI VAVAGVYFYR TRR 453
<212> Type : PRT
<211> Length : 453
SequenceName : SEQ ID 224
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MTFKKLVLGL LSFVAVFTLV ACSSSNSKNL QDDIKEKKKL VVAVSPDYAP FEFKALVNGK 60
DTVVGADIDL AKAIAKELGV KLELSSMSFD NVLSSLKTGK ADIAISGLSY TKERAQAYDF 120
SEAYYKTENA ILIKKSDLNK YTMISSFNNK TKVAVQKGTI EEGLAKNQLK QSNITSLTSM 180
GEAVNELKSG QVDAIDLEKP VAEGYVSQNS DLVLAKVALK TGEGDAKAVA LPKDSGQLVK 240
TVNKVIKKLK KEDKYKQFIS DAVKLTGQQV D 271
<212> Type : PRT
<211> Length : 271
SequenceName : SEQ ID 225
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKHFFMTFS LLLAAVFLVA CSNLSDSGQR NWDKINKRGM LKIATAGTLY PQSYHDDHNK 60
LTGYDVEILK EIGKRLGLKV QFTEMGVDGM LTAIKSGQID VANYSLEDGN KNISKFLRTS 120
PYKYSFTSMV VRSKDDSGIH SWSDLKGKKA AGAASTNYMK IAKKLGAKLV VYDNVTNDVY 180
MKDLVNGRTD VIINDYYLQK IAVAAVKDKY AIKINQGLYA NPYSTSFTLS LKNKVLQKKI 240
NKAVKDMRKD GTLTKLSKKF FQGEDVTKKH YNSYKKIDIS DVD 283
<212> Type : PRT
<211> Length : 283
SequenceName : SEQ ID 226
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKLLKKMMQV ALATFFFGLL GTSTVFADDS EGWQFVQENG RTYYKKGALK ETYWRVIDGK 60
YYYFDPLSGE MVVGWQYIPA PHKGVTIGPS PRIEIALRPD WFYFGQDGVL QEFVGKQVLE 120
AKTATNTNKH HGEEYDSQAE KRVYYFEDQR SYHTLKTGWI YEEGYWYYLQ KDGGFDSRIN 180
RLTVGELARG WVKDYPLTYD EEKLKAAPWY YLDPATGWQN LGNKWYYLRS SGAMATGWYQ 240
EGSTWYYLNA SNGDMKTGWF QVNGNWYYAY DSGALAVNTT VGGYYLNYNG EWVK 294

<212> Type : PRT
<211> Length : 294
SequenceName : SEQ ID 227
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKLLKKMMQV LLAVFFFGLL ATNTVFANTT GGRFVDKDNR KYYVKDDHKA IYWHKIDGKT 60
YYFGDIGEMV VGWQYLEIPG TGYRDNLFDN QPVNEIGLQE KWYYFGQDGA LLEQTDKQVL 120
EAKTSENTGK VYGEQYPLSA EKRTYYFDNN YAVKTGWIYE DGNWYYLNKL GNFGDDSYNP 180
LPIGEVAKGW TQDFHVTIDI DRSKPAPWYY LDASGKMLTD WQKVNGKWYY FGSSGSMATG 240
WKYVRGKWYY LDNKNGDMKT GWQYLGNKWY YLRSSGAMVT GWYQDGLTWY YLNAGNGDMK 300
TGWFQVNGKW YYAYSSGALA VNTTVDGYSV NYNGEWVQ 338
<212> Type : PRT
<211> Length : 338
SequenceName : SEQ ID 228
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MNKKKMILTS LASVAILGAG FVASQPTVVR AEESPVASQS KAEKDYDAAK KDAKNAKKAV 60
EDAQKALDDA KAAQKKYDED QKKTEEKAAL EKAASEEMDK AVAAVQQAYL AYQQATDKAA 120
KDAADKMIDE AKKREEEAKT KFNTVRAMVV PEPEQLAETK KKSEEAKQKA PELTKKLEEA 180
KAKLEEAEKK ATEAKQKVDA EEVAPQAKIA ELENQVHRLE QELKEIDESE SEDYAKEGFR 240
APLQSKLDAK KAKLSKLEEL SDKIDELDAE IAKLEDQLKA AEENNNVEDY FKEGLEKTIA 300
AKKAELEKTE ADLKKAVNEP EKPAPAPETP APEAPAEQPK PAPAPQPAPA PKPEKPAEQP 360
KPEKTDDQQA EEDYARRSEE EYNRLTQQQP PKAEKPAPAP KTGWKQENGM WYFYNTDGSM 420
ATGWLQNNGS WYYLNSNGAM ATGWLQYNGS WYYLNANGAM ATGWAKVNGS WYYLNANGAM 480
ATGWLQYNGS WYYLNANGAM ATGWAKVNGS WYYLNANGAM ATGWLQYNGS WYYLNANGAM 540
ATGWAKVNGS WYYLNANGAM ATGWVKDGDT WYYLEASGAM KASQWFKVSD KWYYVNGLGA 600
LAVNTTVDGY KVNANGEWV 619
<212> Type : PRT
<211> Length : 619
SequenceName : SEQ ID 229
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKILPFIARG TSYYLKMSVK KLVPFLVVGL MLAAGDSVYA YSRGNGSIAR GDDYPAYYKN 60
GSQEIDQWRM YSRQCTSFVA FRLSNVNGFE IPAAYGNANE WGHRARREGY RVDNTPTIGS 120
ITWSTAGTYG HVAWVSNVMG DQIEIEEYNY GYTESYNKRV IKANTMTGFI HFKDLDSGSV 180
GNSQSSASTG GTHYFKTKSA IKTEPLVSAT VIDYYYPGEK VHYDQILEKD GYKWLSYTAY 240
NGSYRYVQLE AVNKNPLGNS VLSSTGGTHY FKIKSAIKTE PLVSATVIDY YYPGEKVHYD 300
QILEKDGYKW LSYTAYNGSR RYIQLEGVTS SQNYQNQSGN ISSYGSNNSS TVGWKKINGS 360
WYHFKSNGSK STGWLKDGSS WYYLKLSGEM QTGWLKENGS WYYLGSSGAM KTGWYQVSGE 420
WYYSYSSGAL AINTTVDGYR VNSDGERV 448
<212> Type : PRT
<211> Length : 448
SequenceName : SEQ ID 230
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MFASKSERKV HYSIRKFSIG VASVAVASLV MGSVVHATEN EGSTQAATSS NMAKTEHRKA 60
AKQVVDEYIE KMLREIQLDR RKHTQNVALN IKLSAIKTKY LRELNVLEEK SKDELPSEIK 120
AKLDAAFEKF KKDTLKPGEK VAEAKKKVEE AKKKAEDQKE EDRRNYPTNT YKTLELEIAE 180
FDVKVKEAEL ELVKEEAKES RNEGTIKQAK EKVESKKAEA TRLENIKTDR KKAEEEAKRK 240
ADAKLKEANV ATSDQGKPKG RAKRGVPGEL ATPDKKENDA KSSDSSVGEE TLPSSSLKSG 300
KKVAEAEKKV EEAEKKAKDQ KEEDRRNYPT NTYKTLDLEI AESDVKVKEA ELELVKEEAK 360
EPRDEEKIKQ AKAKVESKKA EATRLENIKT DRKKAEEEAK RKAAEEDKVK EKPAEQPQPA 420
PATQPEKPAP KPEKPAEQPK AEKTDDQQAE EDYARRSEEE YNRLTQQQPP KTEKPAQPST 480
PKTGWKQENG MWYFYNTDGS MATGWLQNNG SWYYLNANGA MATGWLQNNG SWYYLNANGS 540
MATGWLQNNG SWYYLNANGA MATGWLQYNG SWYYLNSNGA MATGWLQYNG SWYYLNANGD 600
MATGWLQNNG SWYYLNANGD MATGWLQYNG SWYYLNANGD MATGWVKDGD TWYYLEASGA 660
MKASQWFKVS DKWYYVNGSG ALAVNTTVDG YGVNANGEWV N 701
<212> Type : PRT
<211> Length : 701
SequenceName : SEQ ID 231
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKKTTILSLT TAAVILAAYV PNEPILAAYV PNEPILADTP SSEVIKETKV GSIIQQNNIK 60
YKVLTVEGNI GTVQVGNGVT PVEFEAGQDG KPFTIPTKIT VGDKVFTVTE VASQAFSYYP 120
DETGRIVYYP SSITIPSSIK KIQKKGFHGS KAKTIIFDKG SQLEKIEDRA FDFSELEEIE 180
LPASLEYIGT SAFSFSQKLK KLTFSSSSKL ELISHEAFAN LSNLEKLTLP KSVKTLGSNL 240
FRLTTSLKHV DVEEGNESFA SVDGVLFSKD KTQLIYYPSQ KNDESYKTPK ETKELASYSF 300
NKNSYLKKLE LNEGLEKIGT FAFADAIKLE EISLPNSLET IERLAFYGNL ELKELILPDN 360

VKNFGKHVMN GLPKFLTLSG NNINSLPSFF LSGVLDSLKE IHIKNKSTEF SVKKDTFAIP 420
ETVKFYVTSE HIKDVLKSNL STSNDIIVEK VDNIKQETDV AKPKKNSNQG VVGWVKDKGL 480
WYYLNESGSM ATGWVKDKGL WYYLNESGSM ATGWVKDKGL WYYLNESGSM ATGWVKDKGL 540
WYYLNESGSM ATGWVKDKGL WYYLNESGSM ATGWVKDKGL WYYLNESGSM ATGWVKDKGL 600
WYYLNESGSM ATGWVKDKGL WYYLNESGSM ATGWVKDKGL WYYLNESGSM ATGWVKVSGK 660
WYYTYNSGDL LVNTTTPDGY RVNANGEWVG 690
<212> Type : PRT
<211> Length : 690
SequenceName : SEQ ID 232
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MEINVSKLRT DLPQVGVQPY RQVHAHSTGN PHSTVQNEAD YHWRKDPELG FFSHIVGNGC 60
IMQVGPVDNG AWDVGGGWNA ETYAAVELIE SHSTKEEFMT DYRLYIELLR NLADEAGLPK 120
TLDTGSLAGI KTHEYCTNNQ PNNHSDHVDP YPYLAKWGIS REQFKHDIEN GLTIETGWQK 180
NDTGYWYVHS DGSYPKDKFE KINGTWYYFD SSGYMLADRW RKHTDGNWYW FDNSGEMATG 240
WKKIADKWYY FNEEGAMKTG WVKYKDTWYY LDAKEGAMVS NAFIQSADGT GWYYLKPDGT 300
LADRPEFTVE PDGLITVK 318
<212> Type : PRT
<211> Length : 318
SequenceName : SEQ ID 233
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAARA HAAQQNGFEA 60
FAPFAAAVLT AHATGNAGQA TVNTLAGLFI LFRLAFIWCY IADKAALRSL MWVGGFVCTV 120
GLFVVAA 127
<212> Type : PRT
<211> Length : 127
SequenceName : SEQ ID 234
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNKIYRIIWN SALNAWVAVS ELTRNHTKRA SATVKTAVLA TLLFATVQAN ATDEDEEEEL 60
ESVQRSVVGS IQASMEGSGE LETISLSMTN DSKEFVDPYI VVTLKAGDNL KIKQNTNENT 120
NASSFTYSLK KDLTGLINVE TEKLSFGANG KKVNIISDTK GLNFAKETAG TNGDTTVHLN 180
GIGSTLTDTL AGSSASHVDA GNQSTHYTRA ASIKDVLNAG WNIKGVKTGS TTGQSENVDF 240
VRTYDTVEFL SADTKTTTVN VESKDNGKRT EVKIGAKTSV IKEKDGKLVT GKGKGENGSS 300
TDEGEGLVTA KEVIDAVNKA GWRMKTTTAN GQTGQADKFE TVTSGTNVTF ASGKGTTATV 360
SKDDQGNITV MYDVNVGDAL NVNQLQNSGW NLDSKAVAGS SGKVISGNVS PSKGKMDETV 420
NINAGNNIEI SRNGKNIDIA TSMAPQFSSV SLGAGADAPT LSVDDEGALN VGSKDANKPV 480
RITNVAPGVK EGDVTNVAQL KGVAQNLNNR IDNVDGNARA GIAQAIATAG LVQAYLPGKS 540
MMAIGGGTYR GEAGYAIGYS SISDGGNWII KGTASGNSRG HFGASASVGY QW 592

<212> Type : PRT
<211> Length : 592
SequenceName : SEQ ID 235
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MLLAEGQKSA VTEYYLNHGT WPSNNSDAGV ASTATDIKGK YVKEVKVEKG VITATMLSSG 60
VNNEIKGKKL SLWAKRQAGS VKWFCGQPVE RAANNAANDA VTAATANGNG KIDTKHLPST 120
CRDAASAVCI ETPPTAFYKN T 141
<212> Type : PRT
<211> Length : 141

SequenceName : SEQ ID 236
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MKTTDKRTTE THRKAPKTGR IRFSPAYLAI CLSFGILPQA WAGHTYFGIN YQYYRDFAEN 60
KGKFAVGAKD IEVYNKKGEL VGKSMTKAPM IDFSVVSRNG VAALVGDQYI VSVAHNGGYN 120
NVDFGAEGRN PDQHRFSYQI VKRNNYKPDN SHPYNGDYHM PRLHKFVTDA EPVEMTSDMR 180
GNTYSDKEKY PERVRIGSGH HYWRYDDDKH GDLSYSGAWL IGGNTHMQGW GNNGVVSLSG 240
DVRHANDYGP MPIAGAAGDS GSPMFIYDKT NNKWLLNGVL QTGYPYSGRE NGFQLIRKDW 300
FYDDIYRGDT HTVFFEPRSN GHFSFTSNNN GTGTVTETNE KVSNPKLKVQ TVRLFDESLN 360
ETDKEPVYAA GGVNQYRPRL NNGENLSFID YGNGKLILSN NINQGAGGLY FEGDFTVSPE 420
NNETWQGAGV HISEDSTVTW KVNGVANDRL SKIGKGTLHV QAKGENQGSI SVGDGTVILD 480
QQADDKGKKQ AFSEIGLVSG RGTVQLNADN QFNPDKLYFG FRGGRLDLNG HSLSFHRIQN 540
TDEGAMIVNH NATTTSTVTI TGNESITQPS GKNINRLNYS KEIAYNGWFG EKDTTKTNGR 600
LNLVYQPAAE DRTLLLSGGT NLNGNITQTN GKLFFSGRPT PHAYNHLGSG WSKMEGIPQG 660
EIVWDNDWIN RTFKAENFHI QGGQAVISRN VAKVEGDWHL SNHAQAVFGV APHQSHTICT 720
RSDWTGLTNC VEKTITDDKV IASLTKTDIS GNVSLADHAH LNLTGLATLN GNLSANGDTR 780
YTVSHNATQN GNLSLVGNAQ ATFNQATLNG NTSASGNASF NLSNNAAQNG SLTLSDNAKA 840
NVSHSALNGN VSLADKAVFH FENSRFTGQL SGSKDTALHL KDSEWTLPSG TELGNLNLDN 900
ATITLNSAYR HDAAGAQTGS VSDTPRRRSR RSLLSVTPPT SVESRFNTLT VNGKLNGQGT 960
FRFMSELFGY RSDKLKLAES SEGTYTLAVN NTGNEPVSLD QLTVVEGKDN KPLSENLNFT 1020
LQNEHVDAGA WRYQLIRKDG EFRLHNPVKE QELSDKLGKA EAKKQAEKDN AQSLDALIAA 1080
GRDAAEKTES VAEPARQAGG ENVGIMQAEE EKKRVQADKD SALAKQREAE TRPATTAFPR 1140
ARRARRDLPQ PQPQPQPQPQ PQRDLISRYA NSGLSEFSAT LNSVFAVQDE LDRVFAEDRR 1200
NAVWTSGIRD TKHYRSQDFR AYRQQTDLRQ IGMQKNLGSG RVGILFSHNR TENTFDDGIG 1260
NSARLAHGAV FGQYGIGRFD IGISTGAGFS SGSLSDGIGG KIRRRVLHYG IQARYRAGFG 1320
GFGIEPYIGA TRYFVQKADY RYENVNIATP GLAFNRYRAG IKADYSFKPA QHISITPYLS 1380
LSYTDAASGK VRTRVNTAVL AQDFGKTRSA EWGVNAEIKG FTLSLHAAAA KGPQLEAQHS 1440
AGIKLGYRW 1449
<212> Type : PRT
<211> Length : 1449
SequenceName : SEQ ID 237
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNTLQKGFTL IELMIVIAIV GILAAVALPA YQDYTARAQV SEAILLAEGQ KSAVTEYYLN 60
HGEWPSNNTS AGVASSTDIK GKYVQSVEVK NGVVTATMAS SNVNNEIKGK KLSLWAKRQD 120
GSVKWFCGQP VKRNDTATTN DDVKADTAAN GKQIDTKHLP STCRDAASAG 170
<212> Type : PRT
<211> Length : 170
SequenceName : SEQ ID 238
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK DMDLQALHGR 60
KVALYIATMG DQGSGSLTGG RYSIDALIRG EYINSPAVRT DYTYPRYETT AETTSGGLTG 120
LTTSLSTLNA PALSRTQSDG SGSKSSLGLN IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF 180
FLRGIDVVSP ANADTDVFIN IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL 240
IKPKTNAFEA AYKENYALWM GPYKVSKGIK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN 300
SHEGYGYSDE AVRRHRQGQP 320
<212> Type : PRT
<211> Length : 320
SequenceName : SEQ ID 239
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491

<400> PreSequenceString :
MRPIFLSFVL FPILITACST PDKSARWENI GTISNGNIHT YINKDSVRKN GNLMIFQDKK 60
VVTNLKQERF ANTPAYKTAI AEWEIHCNNK TYRLSSLQLF DTKNTEISTQ NYTASSLRPM 120
SILSGTLTEK QYETVCGKKL 140
<212> Type : PRT
<211> Length : 140
SequenceName : SEQ ID 240
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNKLFITALS ALALSACAGT WEGAKQDTAE NLDKTQAAAE RAAEQTGNAV EKGWDKTKEA 60
VKKGGNAVGR GISHLGGKIE NATE 84
<212> Type : PRT
<211> Length : 84
SequenceName : SEQ ID 241
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MKLLFIPLVL FVAVEHFYIA WLEMTQIPSE KAAETFKLPY EFMEQNRVQT LFGNQGLYNG 60
FLGIGLVWSR FAAPDNAVYG ATVLFLGFVL IAAAWGAFSS GNKGILVKQG LPAFLAAAAV 120
LAV 123
<212> Type : PRT
<211> Length : 123
SequenceName : SEQ ID 242
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MASSNVNNEI KDKKLSLWAK RQDGSVKWFC GQPVKRDAAT DADVTADSGN EIDTKHLPST 60
CRDAASAVCT KTPEYYPNHG EWPKNFVIPA QAGIQVCRHG NLSGKKVSPV LSSRFPLSWE 120

<212> Type : PRT
<211> Length : 120
SequenceName : SEQ ID 243
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MLLAEGQKSA VTEYYLNHGE WPSNNTSAGV ATSTDIKGKY VQSVEVKNGV VTATMASSNV 60
NNEIKGKKLS LWAKRQDGSV KWFCGQPVKR NDTATTNDDV KADTAANGKQ IDTKHLPSTA 120
STRKSTPN 128
<212> Type : PRT
<211> Length : 128
SequenceName : SEQ ID 244
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MPIPFKPVLA AAAIAQAFPA FAADPAPQSA QTLNEITVTG THKTQKLGEE KIRRKTLDKL 60
LVNDEHDLVR YDPGISVVEG GRAGSNGFTI RGVDKDRVAI NVDGLAQAES RSSEAFQELF 120
GAYGNFNANR NTSEPENFSE VTITKGADSL KSGSGALGGA VNYQTKSASD YVSEDKPYHL 180
GIKGGSVGKN SQKFSSITAA GRLFGLDALL VYTRRFGKET KNRSTEGDIE IKNDGYVYNP 240
TDTGGPSKYL TYVATGVARS QPDPQEWVNK STLFKLGYNF NDQNRIGWIF EDSRTDRFTN 300
ELSNLWTGTT TSAATGDYRH RQDVSYRRRS GVEYKNELEH GPWDSLKLRY DKQRIDMNTW 360
TWDIPKNYDK RGINGEVYHS FRHIRQNTAQ WTADFEKQLD FSKAVWAAQY GLGGGKGDNA 420

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NSDYSYFAKL YDPKILASNQ AKITMLIENR SKYKFAYWNN AFHLGGNDRF RLNAGIRYDK    480
NSSSAKDDPK YTTAIRGQIP HLGSERAHAG FSYGTGFDWR FTKHLHLLAK YSTGFRAPTS    540
DETWLLFPHP DFYLKANPNL KAEKAKNWEL GLAGSGKAGN FKLSGFKTKY RDFIELTYMG    600
VSSDDKNNPR YAPLSDGTAL VSSPVWQNQN RSAAWVKGIE FNGTWNLDSI GLPKGLHTGL    660
NVSYIKGKAT QNNGKETPIN ALSPWTAVYS LGYDAPSKRW GINAYATRTA AKKPSDTVHS    720
NDDLNNPWPY AKHSKAYTLF DLSAYLNIGK QVTLRAAAYN ITNKQYYTWE SLRSIREFGT    780
VNRVDNKTHA GIQRFTSPGR SYNFTIEAKF                                     810
<212> Type : PRT
<211> Length : 810
      SequenceName : SEQ ID 245
      SequenceDescription :

Sequence
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<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MKKSLIALTL AALPVAAMAD VTLYGTIKTG VETSRSVEHN GGQVVSVETG TGIVDLGSKI     60
GFKGQEDLGN GLKAIWQVEQ KASIAGTDSG WGNRQSFIGL KGGFGKLRVG RLNSVLKDTG    120
DINPWDSKSD YLGVNKIAEP EARLISVRYD SPEFAGLSGS VQYALNDNVG RHNSESYHAG    180
FNYKNGGFFV QYGGAYKRHQ DVDDVKIEKY QIHRLVSGYD NDALYASVAV QQQDAKLVED    240
NSHNSQTEVA ATLAYRFGNV TPRVSYAHGF KGSVDDAKRD NTYDQVVVGA EYDFSKRTSA    300
LVSAGWLQEG KGENKFVATA GGVGLRHKF                                      329
<212> Type : PRT
<211> Length : 329
      SequenceName : SEQ ID 246
      SequenceDescription :

Sequence
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<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MKTLLLLIPL VLTACGTLTG IPAHGGGKRF AVEQELVAAS SRAAVKEMDL SALKGRKAAL     60
YVSVMGDQGS GNISGGRYSI DALIRGGYHN NPESATQYSY PAYDTTATTK SDALSSVTTS    120
TSLLNAPAAA LTKNSGRKGE RSAGLSVNGT GDYRNETLLA NPRDVSFLTN LIQTVFYLRG    180
IEVVPPEYAD TDVFVTVDVF GTVRSRTELH LYNAETLKAQ TKLEYFAVDR DSRKLLIAPK    240
TAAYESQYQE QYALWMGPYS VGKTVKASDR LMVDFSDITP YGDTTAQNRP DFKQNNGKKP    300
DVGNEVIRRR KGG                                                       313
<212> Type : PRT
<211> Length : 313
      SequenceName : SEQ ID 247
      SequenceDescription :

Sequence
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<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNKTLSILPV AILLGGCAAG GGNTFGSLDG GTGMGGSIVK MAVESQCRAE LNKRSEWRLT     60
ALAMSAEKQA EWENKICACV AQEAPNQLTG NDVMQMLDPS TRNQALAALT AKTVSACFKH    120
LYR                                                                  123
<212> Type : PRT
<211> Length : 123
      SequenceName : SEQ ID 248
      SequenceDescription :

Sequence
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<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNPLIHQAKE SSMQTRILSA VLLAFSTAAF AGGAFTLQFD NPSEDGGFTQ NQILSAPYGF     60
GCSGGNASPA LSWKNPPAGT KSFVLTVYDK DAPTGLGWMH WVVADIPADV RRRNATSLQL    120
SRCASIADDQ SAAISAVISL QICRIRLTPS YTAKPMPSCC NHANTPQSAA SAALCGTSSS    180
VSTAAA                                                               186
<212> Type : PRT
<211> Length : 186
      SequenceName : SEQ ID 249
      SequenceDescription :
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Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNKTLKRRVF RHTALYAAIL MFSHTGGGGG AMAQTRQYAI IMNERNQPEV QWNGSYSIKD 60
KDRKREYTHH NHQQGGSSVS FNNSDELVSR QSGTAVFGTA TYLPPYGKVS GFDAAALKER 120
NNAVDWIHTT HPGLIGYSYD GVVCRSATDC PKLVYKTRFS FDNPDLAKTG GGLDKHTEPS 180
RDNSPIYKLK DHPWLGVSFN LGAEGIAKNG KTINKLVSSF NEKNSNNNLV YTTEGRDISL 240
GNWQRETTAM AYYLNAKLHL LDKKQIQNIT DKTVQLGVLK PSIDVRTRNT GTAGILSYWA 300
KWDIKDTGQI PVKLSLTQVK AGRCVNKDNP NKNTKTSSPA LTAPALWFGA GQDGKAEMYS 360
ASVSTYPDSS SSRIFLQNLK RKTDTSRPGR YSLATLNKSD IESREPSFTS RQTVIRLDGG 420
VQQIKLDRNN TEVTGFNGND GKNDTFGIVS EGSFMPDASE WKKVLLPWTV RAFNYDGRFN 480
TVNKEENNGK PKYSQKYRSR NNGKHERNLG DIVNSPIVAV GEYLATSAND GMVHIFKQSG 540
GDKRSYNLKL SYIPGTMPRK DIESKDSTLA KELRAFAEKG YVGDRYGVDG GFVLRRITDD 600
QDKQKHFFMF GAMGLGGRGA YALDLTKADD NDPTKASLFD VKDNGNNGNN GNNRVELGYT 660
VGTPQIGKTH NGKYAAFLAS GYATKQIDSG ENKTALYVVD LESNNGTLIR KIEVTDGKGG 720
LSSPTLVDKD LDGTVDIAYA GDRGGKMYRF DLSGNNPNSW TVRTIFQGTK PITSAPAISQ 780
LKDKRVVIFG TGSDLSEDDV LSTDEQHIYG IFDNDTNTGT AQEGLGKGLL EQKLSEENKT 840
LFLTDYKRSD GSGDKGWVVK LKDGQRVTVK PTVVLRTAFV TIHKYTGNDK CGAETAILGI 900
NTADGGKLTK KSARPIVPAA NSKVAQYSGD KKTSSGKSIP IGCMEKDGGT VCPNGYVYDK 960
PVNVRYLDEK KTDGFSTTAD GDAGGSGTFK EGKKPARNNR CFSGKGVRTL LMNDLDSLDI 1020
TGPMCGMKRI SWREVFY 1037
<212> Type : PRT
<211> Length : 1037
SequenceName : SEQ ID 250
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MKHPKLTLIA ALLTTAATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG ANQDTHAYHM 60
TSGDIKKIRS AKLVLINGLG LEAADIQRAV KQSKVSYAEA TKGIQPLKAE EEGGHHHDHD 120
HDHDHDHEGH HHDHGEYDPH VWNDPVLMSA YAQNVAEALI KADPEGKVYY QQRLGNYQMQ 180
LKKLHSDAQA AFNAVPAAKR KVLTGHDAFS YMGKRYHIEF IAPQGVSSEA EPSAKQVAAI 240
IRQIKREGIK AVFTENIKDT RMVDRIAKET GVNVSGKLYS DALGNAPADT YIGMYRHNIK 300
ALTNAMKQ 308
<212> Type : PRT
<211> Length : 308
SequenceName : SEQ ID 251
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MKKRILSAVL VSGVTLGAAT TVGAEDLSTK IAKQDSIISN LTTEQKAAQN QVSALQAQVS 60
SLQSEQDKLT ARNTELEALS KRFEQEIKAL TSQIVARNEK LKNQARSAYK NNETSGYINA 120
LLNSKSISDV VNRLVAINRA VSANAKLLEQ QKADKVSLEE KQAANQTAIN TIAANMAMAE 180
ENQNTLRTQQ ANLEAATANL ALQLASATED KANLVAQKEA AEKAAAEALA QEQAAKVKAQ 240
EQAAQQAASV EAAKSAITPA PQATPAAQSS NAIEPAALTA PAAPSARPQT SYDSSNTYPV 300
GQCTWGAKSL APWAGNNWGN GGQWAYSAQA AGYRTGSTPM VGAIAVWNDG GYGHVAVVVE 360
VQSASSIRVM ESNYSGRQYI ADHRGWFNPT GVTFIYPH 398
<212> Type : PRT
<211> Length : 398
SequenceName : SEQ ID 252
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MITIKNPKIL KWLKYVLSAI LSLIILVIII GGLLFTFYIS SAPKLSEAQL KSTNSSLVYD 60
GNNNLIADLG SEKRENVTAD SIPINLVNAI TSIEDKRFFN HRGVDLYRIF GAAFHNLTSQ 120
TTQGGSTLDQ QLIKLAYFST NESDQTLKRK AQEVWLALQM ERKYTKQEIL TFYINKVYMG 180
NGNYGMLTAA KSYYGKDLKD LSYAQLALLA GIPQAPSQYD PYLHPEAAQN RRNVVLQQMY 240
MEKHLTKAEY ETAIATPVAE GLQSLQQRST YPKYMDNYLK QVIEEVKKET NKDIFTAGLK 300

VYTNIIPDAQ QTLYNIYHSG DYVYYPDQDF QVASTIVDVT NGHVIAQLGG RNQDENVSFG 360
TNQAVLTDRD WGSTMKPITA YAPAIESGVY TSTAQSTNDS VYYWPGTTTQ LFNWDLRYNG 420
WMTIQAAIML SRNVPAVRAL EAAGLDYARS FLSSLGINYP EMHYSNAISS NNSSSDKKYG 480
ASSEKMAAAY AAFANGGIYH KPRYVNKVEF SDGTSKTFDE KGKRAMKETT AYMMTDMLKT 540
VLTYGTGTAA AIPGVAQAGK TGTSNYTDEE LAKIGEKYGL YPDYVGTLAP DENFVGFTKR 600
YAMAVWTGYK NRLTPVYGSS LEIASDVYRS MMTYLTNGYS EDWTMPNGLY RSGGFLYLSG 660
TYASNTDYTN SVYNNLYSNN TTTASSQTTS DDTSSSNDTS NSTNTDNNGS HPSTDDKKTT 720
H 721
<212> Type : PRT
<211> Length : 721
SequenceName : SEQ ID 253
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MIITKKSLFV TSVALSLAPL VTAQAQEWTP RSVTEIKSEL VLVDNVFTYT VKYGDTLSTI 60
AEAMGIDVHV LGDINHIANI DLIFPDTILT ANYNQHGQAT TLTVQAPASS PASVSHVPSS 120
EPLPQASATS QSTVPMAPSA TPSDVPTTPL ASAKPDSFVT ASSELTSSTN DVSTELSSES 180
QKQPEVSQEA VPTPKAAETT EVEPKTDISE DPTSANRPVP NESASEEASS AAPAQAPAEK 240
EETSQMLTAP AAQKAVADTT SVATSNGLSY APNHAYNPMN AGLQPQTAAF KEEVASAFGI 300
TSFSGYRPGD PGDHGKGLAI DFMVPVSSTL GDQVAQYAID HMAERGISYV IWKQRFYAPF 360
ASIYGPAYTW NPMPDRGSIT ENHYDHVHVS FNA 393
<212> Type : PRT
<211> Length : 393
SequenceName : SEQ ID 254
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MKKKILLMMS LISVFFAWQL TQAKQVLAEG KVKVVTTFYP VYEFTKGVIG NDGDVSMLMK 60
AGTEPHDFEP STKDIKKIQD ADAFVYMDDN METWVSDVKK SLTSKKVTIV KGTGNMLLVA 120
GAGHDHHHED ADKKHEHNKH SEEGHNHAFD PHVWLSPYRS ITVVENIRDS LSKAYPEKAE 180
NFKANAATYI EKLKELDKDY TAALSDAKQK SFVTQHAAFG YMALDYGLNQ ISINGVTPDA 240
EPSAKRIATL SKYVKKYGIK YIYFEENASS KVAKTLAKEA GVKAAVLSPL EGLTKKEMKA 300
GQDYFTVMRK NLETLRLTTD VAGKEILPEK DTTKTVYNGY FKDKEVKDRQ LSDWSGSWQS 360
VYPYLQDGTL DQVWDYKAKK SKGKMTAAEY KDYYTTGYKT DVEQIKINGK KKTMTFVRNG 420
EKKTFTYTYA GKEILTYPKG NRGVRFMFEA KEPNAGEFKY VQFSDHAIAP EKAEHFHLYW 480
GGDSQEKLHK ELEHWPTYYG SDLSGREIAQ EINAH 515
<212> Type : PRT
<211> Length : 515
SequenceName : SEQ ID 255
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MKKFHRFLVS GVILLGFNGL VPTMPSTLIS QQENLVHAAV LGDNYPSKWK KGNGIDSWNM 60
YIRQCTSFAA FRLSSANGFQ LPKGYGNACT WGHIAKNQGY PVNKTPSIGA IAWFDKNAYQ 120
SNAAYDHVAW VADIRGDTVT IEEYNYNAGQ GPERYHKRQI PKSQVSGYIH FKDLSSQTSH 180
SYPRQLKHIS QASFDPSGTY HFTTRLPVKG QTSIDSPDLA YYEAGQSVYY DKVVTAGGYT 240
WLSYLSFSGN RRYIPIKEPA QSVVQNDNTK PSIKVGDTVT FPGVFRVDQL VNNLIVNKEL 300
AGGDPTPLNW IDPTPLDETD NQGKVLGNQI LRVGEYFTVT GSYKVLKIDQ PSNGIYVQIG 360
SRGTWVNADK ANKL 374
<212> Type : PRT
<211> Length : 374
SequenceName : SEQ ID 256
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :

MLKFTSNILA TSVAETTQVA PGGCCCCCTT CCFSIATGSG NSQGGSGSYT PGK

<212> Type : PRT
<211> Length : 53
SequenceName : SEQ ID 257
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MGESYSVEAV LTAVDKTFGK TLQSAIRSIE GLEKRSTGFS SVSQKASSMF KSMLGANLAG 60
QAISAMTRTV SSGLGSMLGE MNSSAKAWKT FDANLADIGF GKKQILAVKT AMQDYATKTI 120
YSASDMASTY AQLAAVGVKD TGKLVKAFGG LAASAENPKQ AMKSISQQMT QAVGRPTVAW 180
QDFRIMLEQT PAGMAKVAKS MGKNLDELVA DIQAGRVKTS DFLEAVKKAG NDKSFQKMAT 240
EFKTVDQAID GMREGLSNKL QPAFEKVNQF GIRAIEAIGK QLDKVDFSKF ASNLGKFLEG 300
INIDKIVSNI SSAVSSVTSK VKEFWDGFKQ TGAISAFSGA LQSVWGALKN VASAMSGGNW 360
KTFGATVGGI VKHVSNFAKA VSDVLGKMDP GRLRSWIATF AAVAGGFKLF EKLTGQSVIG 420
SFLDKIGSKF GLFGNKAKEG TDKASNGARR SGGIISQIFS GLGNIVKSAG TAISTAAKGI 480
GVGIKTALSG IPPYH 495
<212> Type : PRT
<211> Length : 495
SequenceName : SEQ ID 258
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MKKGFFLMVM VVSLVMIAGC DKSANPKQPT QGMSVVTSFY PMYAMTKEVS GDLNDVRMIQ 60
SGAGIHSFEP SVNDVAAIYD ADLFVYHSHT LEAWARDLDP NLKKSKVDVF EASKPLTLDR 120
VKGLEDMEVT QGIDPATLYD PHTWTDPVLA GEEAVNIAKE LGRLDPKHKD SYTKNAKAFK 180
KEAEQLTEEY TQKFKKVRSK TFVTQHTAFS YLAKRFGLKQ LGISGISPEQ EPSPRQLKEI 240
QDFVKEYNVK TIFAEDNVNP KIAHAIAKST GAKVKTLSPL EAAPSGNKTY LENLRANLEV 300
LYQQLK 306
<212> Type : PRT
<211> Length : 306
SequenceName : SEQ ID 259
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MEKKQRFSLR KYKSGTFSVL IGSVFLMMTT TVAADELSTM SEPTITNHTQ QQAQHLTNTE 60
LSSAESKSQD TSQITPKTNR EKEQPQGLVS EPTTTELADT DAAPMANTGP DATQKSASLP 120
PVNTDVHDWV KTKGAWDKGY KGQGKVVAVI DTGIDPAHQS MRISDVSTAK VKSKEDMLAR 180
QKAAGINYGS WINDKVVFAH NYVENSDNIK ENQFEDFDED WENFEFDAEA EPKAIKKHKI 240
YRPQSTQAPK ETVIKTEETD GSHDIDWTQT DDDTKYESHG MHVTGIVAGN SKEAAATGER 300
FLGIAPEAQV MFMRVFANDV MGSAESLFIK AIEDAVALGA DVINLSLGTA NGAQLSGSKP 360
LMEAIEKAKK AGVSVVVAAG NERVYGSDHD DPLAINPDYG LVGSPSTGRT PTSVAAINSK 420
WVIQRLMTVK ELENRADLNH GKAIYSESVD FKNIKDSLGY DKSHQFAYVK ESTDAGYKAQ 480
DVKDKIALIE RDPNKTYDEM IALAKKHGAL GVLIFNNKPG QSNRSMRLTA NGMGIPSAFI 540
SHEFGKAMSQ LNGNGTGSLE FDSVVSKAPS QKGNEMNHFS NWGLTSDGYL KPDITAPGGD 600
IYSTYNDNHY GSQTGTSMAS PQIAGASLLV KQYLEKTQPN LPKEKIADIV KNLLMSNAQI 660
HVNPETKTTT SPRQQGAGLL NIDGAVTSGL YVTGKDNYGS ISLGNITDTM TFDVTVHNLS 720
NKDKTLRYDT ELLTDHVDPQ KGRFTLTSRS LKTYQGGEVT VPANGKVTVR VTMDVSQFTK 780
ELTKQMSNGY YLEGFVRFRD SQDDQLNRVN IPFVGFKGQF ENLAVAEESI YRLKSQGKTG 840
FYFDESGPKD DIYVGKHFTG LVTLGSETNV STKTISDNGL HTLGTFKNAD GKFILEKNAQ 900
GNPVLAISPN GDNNQDFAAF KGVFLRKYQG LKASVYHASD KEHKNPLWVS PESFKGDKNF 960
NSDIRFAKST TLLGTAFSGK SLTGAELPDG YYHYVVSYYP DVVGAKRQEM TFDMILDRQK 1020
PVLSQATFDP ETNRFKPEPL KDRGLAGVRK DSVFYLERKD NKPYTVTIND SYKYVSVEDN 1080
KTFVERQADG SFILPLDKAK LGDFYYMVED FAGNVAIAKL GDHLPQTLGK TPIKLKLTDG 1140
NYQTKETLKD NLEMTQSDTG LVTNQAQLAV VHRNQPQSQL TKMNQDFFIS PNEDGNKDFV 1200
AFKGLKNNVY NDLTVNVYAK DDHQKQTPIW SSQAGASASA IESTAWYGIT ARGSKVMPGD 1260
YQYVVTYRDE HGKEHQKQYT ISVNDKKPMI TQGRFDTING VDHFTPDKTK ALGSSGIVRE 1320
EVFYLAKKNG RKFDVTEGKD GITVSDNKMY IPKNPDGSYT ISKRDGVTLS DYYYLVEDRA 1380

GNVSFATLRD LKAVGKDKAV VNFGLDLPVP EDKQIVNFTY LVRDADGKPL ENLEYYNNSG 1440
NSLILPYGKY TVELLTYDTN AAKLESDKIV SFTLSADNNF QQVTFKMTML ATSQITAHFD 1500
HLLPEGSRVS LKTAQGQLIP LEQSLYVPKA YGKTVQEGTY EVVVSLPKGY RIEGNTKVNT 1560
LPNEVHELSL RLVKVGDASD STGDHKVMSK NNSQALTAFA TPTKTTTSAT AKALPSAGEK 1620
MGLKLRIVGL VLLGLTCVFS RKKSTKD 1647
<212> Type : PRT
<211> Length : 1647
SequenceName : SEQ ID 260
SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :
MMRSLFSGVS GMQNHQTRMD VIGNNVANVN TTGFKRGRVN FQDLISQQLS AAARPNEEVG 60
GVNPKEVGLG VLIASIDTVH TQGALQTTGI NTDVSIQGSG FFVLKSGEKT FFTRAGAFGV 120
DNAGTLVNPA NGMRVQGWMA QDVAGERLIN SSAQTQDLVI PIGQKIDAQQ TSTVHYACNL 180
DKRLPELAAD ANEADVRKST WTTDFQVYDS FGQQHTLQIN FSRVPGTNNQ WQATVAVDPG 240
TEVDTQTRVG VGTSDGAANT FIVNFDNFGH LASVTDTAGN VTGPTGQVLL EASYDVVGAN 300
PDDAGQVTRH AFTLNLGEIG TARNTITQFA ERSTTKAYRQ DGYAMGYLEN FKIDQSGVIT 360
GVYSNGVSQD IGQLALAGFA NQGGLEKAGE NTYVQSNNSG IANISTSGVM GKGKLIAGTL 420
EMSNVDLTDQ FTDMIITQKG FQAGAKTIQT SDTMLDTVLS LKR 463
<212> Type : PRT
<211> Length : 463
SequenceName : SEQ ID 261
SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :
MGCMRWGSVL CVVVGVGASG GVLGQEFSPK LTGSATLEWG ISYGKGVGSH GQAPGAVMGT 60
GPYNLKHGFR TTNTVGVSFP LVMRTTHTRR GQHPALYAEL KVADLQADLS QGKAGFAVKR 120
KGKVEATLHC YGAYLTIGKN PTFLTNFARL WKPWVTAQYQ EDAVQYAPGF GGLGGKVGYR 180
AQDIGGSGVS LDVGFLSFAS NGAWDSTDPT HSKYGFGADL KLMYARAGHP LCTVELASNV 240
TLEDGYLIGA QKDANNQNKD KLLWNVGGRL TLEPGAGFRF SFALDAGNQH QSAQDFQNRT 300
QRAQSELTAL SNNLFQGESQ KQEAWVTQVV QQATQTVTAG VRSALESRGT TYINALEAVQ 360
PNPAKPTGKV VQNLHTPQGS PPNLPPLPAL PAFSLMGQVL LQYDAEQVVK GFEQVQTQIV 420
TEINQKVQAA VAKNNANMQA VGGSLGDTAR MVGEALIKQQ LSRKQNSILT MVSVQDEVKQ 480
DLADLVPMMR TEITAFFASV QQHITEEVKK KTDALNAGQQ IRQAIQNLRA SAWRAFLMGV 540
SAVCLYLDTY NVAFDALFTA QWKWLSSGIY FATAPANVFG TRVLDNTIAS CGDFAGFLKL 600
ETKSGDPYTH LLTGLDAGVE TRVYIPLTHD LYKNNNGNPL PSGGSSGHIG LPVVGKAWCS 660
YRIPVQDYGW VKPSVTVHAS TNRAHLNAPA AGGAVGATYL TKEYCAQLRA GISASLIEKT 720
VFSLDWEQGM LSDVPYLLVS ECLTQGIGRI VCGVTLSW 758
<212> Type : PRT
<211> Length : 758
SequenceName : SEQ ID 262
SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :
MGRQVMQAGV LAGMVCAASG YAGVLTPQVS GTAQLQWGIA FQKNPRTGPG KHTHGFRTTN 60
SLTISLPLVS KHTHTRRGEA RSGVWAQLQL KDLAVELASS KSSTALSFTK PTASFQATLH 120
CYGAYLTVGT SPSCVVNFAQ LWKPFVTRAY SEKDTRYAPG FSGSGAKLGY QAHNVGNSGV 180
DVDIGFLSFL SNGAWDSTDT THSKYGFGAD ATLSYGVDRQ RLLTLELAGN ATLDQNYVKG 240
TEDSKNENKT ALLWGVGGRL TLEPGAGFRF SFALDAGNQH QSNAHAQTQE RAILKAREVF 300
RRVEGKLVQN LPNIMMPPGI TEQTTLIEMV GLAALIAEGT LGSAIQTVLA AGALAALVSQ 360
LVPNIEQGVR DVFRSSDPRV VTAKLLAFLE RAPMNALNID ALLRMQWKWL SSGIYFATAG 420
TNIFGKRVFA TTRAHYFDFA GFLKLETKSG DPYTHLLTGL NAGVEARVYI PLTYIRYRNN 480
GGYELNGAVP PGTINMPILG KAWCSYRIPL GSHAWLAPHT SVLGTTNRFN IINPAGNLLN 540
ERALQYQVGL TFSPFEKVEL SAQWEQGVLA DAPYMGIAES IWSERHFGTL VCGMKVTW 598

<212> Type : PRT
<211> Length : 598
SequenceName : SEQ ID 263

SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum subsp. pallidum str. Nichols
<400> PreSequenceString :
MGRQVMQAGV LAGMVCAASG YAGVLTPQVS GTAQLQWGIA FQKNPRTGPG KHTHGFRTTN 60
SLTISLPLVS KHTHTRRGEA RSGVWAQLQL KDLAVELASS KSSTALSFTK PTASFQATLH 120
CYGAYLTVGT SPSCVVNFAQ LWKPFVTRAY SEKDTRYAPG FSGSGAKLGY QAHNVGNSGV 180
DVDIGFLSFL SNGAWDSTDT THSKYGFGAD ATLSYGVDRQ RLLTLELAGN ATLDQNYVKG 240
TEDSKNENKT ALLWGVGGRL TLEPGAGFRF SFALDAGNQH QSNAHAQTQE RAILKAREVF 300
RRVEGKLVQN LPNIMMPPGI TEQTTLIEMV GLAALIAEGT LGSAIQTVLA AGALAALVSQ 360
LVPNIEQGVR DVFRSSDPRV VTAKLLAFLE RAPMNALNID ALLRMQWKWL SSGIYFATAG 420
TNIFGKRVFA TTRAHYFDFA GFLKLETKSG DPYTHLLTGL NAGVEARVYI PLTYIRYRNN 480
GGYELNGAVP PGTINMPILG KAWCSYRIPL GSHAWLAPHT SVLGTTNRFN IINPAGNLLN 540
ERALQYQVGL TFSPFEKVEL SAQWEQGVLA DAPYMGIAES IWSERHFGTL VCGMKVTW 598

<212> Type : PRT
<211> Length : 598
SequenceName : SEQ ID 264
SequenceDescription :

Sequence

<213> OrganismName : SARS coronavirus Frankfurt 1
<400> PreSequenceString :
MFIFLLFLTL TSGSDLDRCT TFDDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLFL 60
PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDFGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 265
SequenceDescription :

Sequence

<213> OrganismName : SARS coronavirus HSR 1
<400> PreSequenceString :
MFIFLLFLTL TSGSDLDRCT TFDDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLFL 60
PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600

VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 266
SequenceDescription :

Sequence

<213> OrganismName : SARS coronavirus ZJ01
<400> PreSequenceString :
MFIFLLFLTL TSGSDLDRCT TFDDVQAPNY TQHTSSMRGV YYPDEIFRSD TLYLTQDLFL 60
PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 267
SequenceDescription :

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<213> OrganismName : SARS coronavirus TW1
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TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900

NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 268
SequenceDescription :

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<213> OrganismName : SARS coronavirus CUHK-Su10
<400> PreSequenceString :
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TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT 1255

<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 269
SequenceDescription :

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<213> OrganismName : SARS coronavirus Urbani
<400> PreSequenceString :
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PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS 120
TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK 180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP 240
AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY 300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF 360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV 420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND 480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP 540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD 600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY 660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC 720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG 780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL 840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE 900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN 960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK 1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN 1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN 1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL 1200

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<212> Type : PRT
<211> Length : 1255
      SequenceName : SEQ ID 270
      SequenceDescription :

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<213> OrganismName : SARS coronavirus
<400> PreSequenceString :
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PFYSNVTGFH TINHTFGNPV IPFKDGIYFA ATEKSNVVRG WVFGSTMNNK SQSVIIINNS     120
TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK     180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP     240
AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY     300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF     360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV     420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND     480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP     540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCAFGG VSVITPGTNA SSEVAVLYQD     600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY     660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC     720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG     780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL     840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE     900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN     960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK    1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN    1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN    1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL    1200
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<212> Type : PRT
<211> Length : 1255
      SequenceName : SEQ ID 271
      SequenceDescription :

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<213> OrganismName : SARS coronavirus Tor2
<400> PreSequenceString :
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TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK     180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP     240
AQDIWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY     300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF     360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV     420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND     480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP     540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCAFGG VSVITPGTNA SSEVAVLYQD     600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY     660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC     720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG     780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL     840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE     900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN     960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK    1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN    1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN    1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL    1200
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<212> Type : PRT
<211> Length : 1255
      SequenceName : SEQ ID 272
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SequenceDescription :

Sequence

<213> OrganismName : SARS coronavirus GD01
<400> PreSequenceString :

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TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK   180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFLP   240
AQDTWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY   300
QTSNFRVVPS RDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKRISNCVA DYSVLYNSTF   360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV   420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND   480
YGFYTTTGIG YQPYRVVVLS YELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP   540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD   600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY   660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC   720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKDFG   780
GFNFSQILPD PLKSTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL   840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE   900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN   960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK  1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN  1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN  1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL  1200
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<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 273
SequenceDescription :

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<213> OrganismName : SARS coronavirus CUHK-W1
<400> PreSequenceString :

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TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK   180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP   240
AQDTWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY   300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF   360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV   420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND   480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP   540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD   600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY   660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC   720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG   780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL   840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE   900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN   960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK  1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN  1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN  1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL  1200
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<212> Type : PRT
<211> Length : 1255
SequenceName : SEQ ID 274
SequenceDescription :

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<213> OrganismName : SARS coronavirus BJ01

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<400> PreSequenceString :
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TNVVIRACNF ELCDNPFFAV SKPMGTQTHT MIFDNAFNCT FEYISDAFSL DVSEKSGNFK    180
HLREFVFKNK DGFLYVYKGY QPIDVVRDLP SGFNTLKPIF KLPLGINITN FRAILTAFSP    240
AQDTWGTSAA AYFVGYLKPT TFMLKYDENG TITDAVDCSQ NPLAELKCSV KSFEIDKGIY    300
QTSNFRVVPS GDVVRFPNIT NLCPFGEVFN ATKFPSVYAW ERKKISNCVA DYSVLYNSTF    360
FSTFKCYGVS ATKLNDLCFS NVYADSFVVK GDDVRQIAPG QTGVIADYNY KLPDDFMGCV    420
LAWNTRNIDA TSTGNYNYKY RYLRHGKLRP FERDISNVPF SPDGKPCTPP ALNCYWPLND    480
YGFYTTTGIG YQPYRVVVLS FELLNAPATV CGPKLSTDLI KNQCVNFNFN GLTGTGVLTP    540
SSKRFQPFQQ FGRDVSDFTD SVRDPKTSEI LDISPCSFGG VSVITPGTNA SSEVAVLYQD    600
VNCTDVSTAI HADQLTPAWR IYSTGNNVFQ TQAGCLIGAE HVDTSYECDI PIGAGICASY    660
HTVSLLRSTS QKSIVAYTMS LGADSSIAYS NNTIAIPTNF SISITTEVMP VSMAKTSVDC    720
NMYICGDSTE CANLLLQYGS FCTQLNRALS GIAAEQDRNT REVFAQVKQM YKTPTLKYFG    780
GFNFSQILPD PLKPTKRSFI EDLLFNKVTL ADAGFMKQYG ECLGDINARD LICAQKFNGL    840
TVLPPLLTDD MIAAYTAALV SGTATAGWTF GAGAALQIPF AMQMAYRFNG IGVTQNVLYE    900
NQKQIANQFN KAISQIQESL TTTSTALGKL QDVVNQNAQA LNTLVKQLSS NFGAISSVLN    960
DILSRLDKVE AEVQIDRLIT GRLQSLQTYV TQQLIRAAEI RASANLAATK MSECVLGQSK   1020
RVDFCGKGYH LMSFPQAAPH GVVFLHVTYV PSQERNFTTA PAICHEGKAY FPREGVFVFN   1080
GTSWFITQRN FFSPQIITTD NTFVSGNCDV VIGIINNTVY DPLQPELDSF KEELDKYFKN   1140
HTSPDVDLGD ISGINASVVN IQKEIDRLNE VAKNLNESLI DLQELGKYEQ YIKWPWYVWL   1200
GFIAGLIAIV MVTILLCCMT SCCSCLKGAC SCGSCCKFDE DDSEPVLKGV KLHYT        1255

<212> Type : PRT
<211> Length : 1255
      SequenceName : SEQ ID 275
      SequenceDescription :

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<213> OrganismName : SARS coronavirus
<400> PreSequenceString :
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SPSGVYQCAM RPNHTIKGSF LNGSCGSVGF NIDYDCVSFC YMHHMELPTG VHAGTDLEGK    180
FYGPFVDRQT AQAAGTDTTI TLNVLAWLYA AVINGDRWFL NRFTTTLNDF NLVAMKYNYE    240
PLTQDHVDIL GPLSAQTGIA VLDMCAALKE LLQNGMNGRT ILGSTILEDE FTPFDVVRQC    300
SGVTFQ                                                              306
<212> Type : PRT
<211> Length : 306
      SequenceName : SEQ ID 276
      SequenceDescription :

Sequence
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<213> OrganismName : SARS coronavirus
<400> PreSequenceString :
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PLTTAAKLMV VVPDYGTYKN TCDGNTFTYA SALWEIQQVV DADSKIVQLS EINMDNSPNL    180
AWPLIVTALR ANSAVKLQ                                                 198
<212> Type : PRT
<211> Length : 198
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      SequenceDescription :

Sequence
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<213> OrganismName : SARS coronavirus
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<212> Type : PRT
<211> Length : 139
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<213> OrganismName : SARS coronavirus
<400> PreSequenceString :
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<212> Type : PRT
<211> Length : 113
      SequenceName : SEQ ID 279
      SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
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SMAFGVSAIS EGDRSIALGA SSYSLGQYSM ALGRYSKALG KLSIAMGDSS KAEGANAIAL     180
GNATKATEIM SIALGDTANA SKAYSMALGA SSVASEENAI AIGAETEAAE NATAIGNNAK     240
AKGTNSMAMG FGSLADKVNT IALGNGSQAL ADNAIAIGQG NKADGVDAIA LGNGSQSRGL     300
NTIALGTASN ATGDKSLALG SNSSANGINS VALGADSIAD LDNTVSVGNS SLKRKIVNVK     360
NGAIKSDSYD AINGSQLYAI SDSVAKRLGG GAAVDVDDGT VTAPTYNLKN GSKNNVGAAL     420
AVLDENTLQW DQTKGKYSAA HGTSSPTASV ITDVADGTIS ASSKDAVNGS QLKATNDDVE     480
ANTANIATNT SNIATNTANI ATNTTNITNL TDSVGDLQAD ALLWNETKKA FSAAHGQDTT     540
SKITNVKDAD LTADSTDAVN GSQLKTTNDA VATNTTNIAN NTSNIATNTT NISNLTETVT     600
NLGEDALKWD KDNGVFTAAH GTETTSKITN VKDGDLTTGS TDAVNGSQLK TTNDAVATNT     660
TNIATNTTNI SNLTETVTNL GEDALKWDKD NGVFTAAHGN NTASKITNIL DGTVTATSSD     720
AINGSQLYDL SSNIATYFGG NASVNTDGVF TGPTYKIGET NYYNVGDALA AINSSFSTSL     780
GDALLWDATA GKFSAKHGTN GDASVITDVA DGEISDSSSD AVNGSQLHGV SSYVVDALGG     840
GAEVNADGTI TAPTYTIANA DYDNVGDALN AIDTTLDDAL LWDADAGENG AFSAAHGKDK     900
TASVITNVAN GAISAASSDA INGSQLYTTN KYIADALGGD AEVNADGTIT APTYTIANAE     960
YNNVGDALDA LDDNALLWDE TANGGAGAYN ASHDGKASII TNVANGSISE DSTDAVNGSQ    1020
LNATNMMIEQ NTQIINQLAG NTDATYIQEN GAGINYVRTN DDGLAFNDAS AQGVGATAIG    1080
YNSVAKGDSS VAIGQGSYSD VDTGIALGSS SVSSRVIAKG SRDTSITENG VVIGYDTTDG    1140
ELLGALSIGD DGKYRQIINV ADGSEAHDAV TVRQLQNAIG AVATTPTKYF HANSTEEDSL    1200
AVGTDSLAMG AKTIVNGDKG IGIGYGAYVD ANALNGIAIG SNAQVIHVNS IAIGNGSTTT    1260
RGAQTNYTAY NMDAPQNSVG EFSVGSADGQ RQITNVAAGS ADTDAVNVGQ LKVTDAQVSQ    1320
NTQSITNLDN RVTNLDSRVT NIENGIGDIV TTGSTKYFKT NTDGVDASAQ GKDSVAIGSG    1380
SIAAADNSVA LGTGSVATEE NTISVGSSTN QRRITNVAAG KNATDAVNVA QLKSSEAGGV    1440
RYDTKADGSI DYSNITLGGG NGGTTRISNV SAGVNNNDVV NYAQLKQSVQ ETKQYTDQRM    1500
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<212> Type : PRT
<211> Length : 1588
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<213> OrganismName : Escherichia coli O157:H7
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TNGVGNTGSG SRDITIDANL PGLRVDTVAG DDVVNSIEHA QALVITGSSS GLAAGAALTV     180
VINTVTYAAT VLADGTWSVG VPAADVSNWP AGTVNITVSG TNTAGTTSTI THPVTVDLAA     240
VAISINTVSG DDVINAAEKG ADLTLSGSTS GVEVGQTVTV TFGGKTYTAT VAGDGSWTTT     300
VPAADLSVLR DGDATVQASV STINGNTASA THAYSVDATA PTLAINTIAT DDILNAAEAG     360
NPLTISGSST AEAGQTVTVT LNGVTYSGSV QADGSWSVSL PTADLSNLTA SQYTVSASVS     420
DKAGNPASAN HGLAVDLTVP VLTINTVSGD DIINAAEHGQ ALVISGSSTG GEAGDVITVT     480
LNSKTYTTML DASGNWSVGV PAADVTALGS GPQTITAAIT DAAGNSDDAS RTVTVNLAAP     540
TIGINTIATD DVIKATEKGA DLQITGTSNQ PAGTTITVTL NGQNYTATTD SNGNWSATVP     600
ASAVSALGEA NYTVTANVTD TAGNSNSASH NVLVNSALPA VTINAVATDD IINAAESGNA     660
QTISGQVTGA AQGDTVTVTL GGNTYTATVQ SNLSWSVDVP AADIQALGNG DLTVNASVTN     720
GVGNTGSGSR DITIDANLPG LRVDTVAGDD VINSIEHNQA LVITGSSSGL TAGTALTVEI     780
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NNVTYGATVL ADGTWSLGVP AVDVSNWPAG TVNITVSGTN SAGTTSTITH PVTVDLAGVA 840
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ITISGTTTAQ AGQTLTVTLN NNTYQTTVLA DGTWSVNVPA ADLSGLTASS YTVTATVSDK 1020
AGNPASADHA LVVDITAPDL TINTVAGDDI INAIEHGQAL VVSGTSTGAA AGDVVTVTLN 1080
GKNYTTTLDA SGNWSVGIPA ADVTALATGS QTITASLSDR AGNSDSTTHD VTVDLSGPTL 1140
TINTVSGDDI INAAEIVVAQ TISGQVTGTA VAGNTVIVTI GGNQYNATVQ SDLSWSVSVP 1200
ANVLQALGNG ELTISASLTN SANNTGTATH DIVIDANLPG LRVDTVAGDD VINSIEHTQA 1260
LVITGSSSGL AAGAALTVVI NSVTYGATVL ADGSWSVGVP VADVTNWPAG TVNIAVSGTN 1320
TAGTTTSISH PVTVDLAAVA ITINTLSTDD VINAAEKGSD LQLSGTTSGV EAGQTITVIF 1380
GGKSYTTTVA ADNTWGLTIP AVDVATLPDG AANVQASVSN VAGNSTQATH AYSVDATAPS 1440
VTINTIATDD ILNAAEAGSA LTISGTSTAE AGQTVTVTLN GVNYSGNVQA DGSWSVSVPT 1500
GDLASLTASS YTVNASVSDK ARNSASATHN LTVDLAAPVV TINTVAGDDI INATEHGQAQ 1560
IISGSATGAT TGNTVSVTIG TTTYTTVLDA NGNWSIGVPA SVISALAQGD VTITATVTDS 1620
AGNSGTASHT VTVALGAPVL AINTIAVDDI INAAEKGADL AITGTSNQPA GTQITVTLNG 1680
QNYTTTADAS GNWSVTVPAS RVSALGEATY TVTAAATDAD GNSGSASHNV QVNTALPGVT 1740
INVVATDDII NAAEAGVEQT ISGQVTGAAA GDTVTVTLGG ATYTATVQAN LSWSVDVPAS 1800
ALQELGNGEL TISASVTNSV GNTGNGTREI TIDANLPGLR VDTVAGDDVV NIIEHGQALV 1860
ITGSSSGLAA GSNVTLTING QTYVAAVLAD GTWSVGVPAV DVSAWPAGSV TIAASGSTSA 1920
GNPVSVTHPV TVDLSAVAVS INAITADDVI NAAEKGAALT LSGGSTSGVEA GQTVTVTFGG 1980
KTYSATVAAN GSWSTSVPAA DMAALRDGDA SAQASVSNVN GNSATTTHAY SVDASAPTVT 2040
INTIAGDDIL NAAEAGAALT ITGSSTAEAG QTVTVTLNGT NYTGTVQTDG SWSVSVPSAD 2100
LSTLTASNYT VNAAVSDKAG NPASVNHNLT VDTSVPVVTI NTVAGDDVIN ATEHAQAQII 2160
SGSATGAATG STVTVTIGTN TFTTVLDASG NWSVGVPASV VSALANGTVT INASVTDAGG 2220
NSGSATHQVT VNTGLPTITF NAISGDNILN ADEKGQPLTI SGGSTGLATG AQVTVTLNGH 2280
NYSATTDASG NWTLTVPVSD LAALGQANYT VSASATSAAG NTASSQANLL VDSGLPDVTI 2340
NTVAGDDIIN AAEAGADQTI SGVVTRAAAG DTVTVTLGGN TYTATVQSNL SWSVSVPTAD 2400
LQALGNGDLT ITASVTNANG NTGSGTRDIT IDANLPGLRV DTVAGDDIVN SIEHGQALVI 2460
TGGSSGLNAG AVLTVTINSV AYSATVQADG SWSVGIPAAN VSAWPAGPLT VEVDGQSSAN 2520
NPVSVSHPFT VDLTAVAISI NTVASDDVIN AAEKGTNLTL SGGSTSGIESG QTVTVTFGGK 2580
TYTASVAANG SWSVNVPAAD LATLPEGAAN VQASVSSASG NSASATHAYS VDASAPTLTI 2640
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GALNASNYTV SATVNDKAGN PGSASHNLAV DTTAPVLTIN TVAGDDIIND AEHAQALVIS 2760
GTSSGGEAGD VVSVVLNGKT YTTTLDASGN WSVGVPAADV TALGSGAQTI TASVSDRAGN 2820
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VATDDIINAS EAGSAQTISG QVTGAAAGST VTVELGGKTY TATVQADLSW NVSVPAADWQ 3000
ALGNGELTVN ASVTNAVGNT GSGTRDITID ASLPGLRVDT VAGDDVVNII EHAQAQVITG 3060
SSSGFAAGTA LTVVINNQTY AATVLANGSW SVGVPATDVS NWPAGTLNIT VSGANSAGTQ 3120
TSITHPLTVD LTAVAISMNS ITSDDAINAA EKGAALTLSG STSGVEAGQT VTVTFGGKTY 3180
TTTVAANGSW STTVPAADLA ALRDGDASAQ VRVTNVNGNS ATATHEYSVD SAAPTVTINT 3240
IASDNIINAS EAAAGVTVSG TSTAQTGQTL TVTLNGTNYQ TTVQTDGSWS LTLPASDLTA 3300
LANNGYTLTA TVSDLAGNLG SASKGVTVDT TAPVISFNTV AGDDVINNVE HIQAQIISGT 3360
ATGAVAGDRL VVTIAGQQYV TSTDASGNWS VGVPASVISG LADGTVTISA TITDSAGNSS 3420
TQTHNVQVNT AAVSLSVSTI SGDNLINAAE AGSALTLSGT GTNFATGTVV TVLLNGKGYS 3480
ATIQSNGSWS VNVPAADVAA LSDGTSYTVS ASAQDSAGNG NSSTQTHNVQ VNTAAVSLSV 3540
STISGDNLIN AAEAGSALTL SGTGTNFATG TVVTVLLNGK GYSATIQSNG SWSVNVPAAD 3600
VAALSDGTSY TVSASAQDSA GNSATASRSV AVDLTAPVIS INTVSTDDRL NAAEQQQPLT 3660
LNGSTSAEVG QTVTVTFGGK TYTATVAANG TWALNVPAVD LAALGQGAQT ITASVNDRAG 3720
NPGQATHALT VDTVAPTVTI ATVAGDDIIN NAEQLAGQTI SGTTTAEVGQ TVTVTFNGQT 3780
WSATVGSGGS WSVFIPAQQF AGLSDGSYTI SATVSDQAGN PGSASRGVTL NGDVPTVTIN 3840
TFAGDDVVNA AEHGSSLVIS GTTTAPVGQT LTLTLNGKTY TTTVQTGGSW SYTLGSADVT 3900
ALADGNAYVI NASVSNAIGN TGSSNHTITV DLSAPAMGIN IDSLQADTGL SASDFITSVS 3960
PVVVNGSLTA ALASNETAQI SIDGGTTWTT LTVTGTTWRY NDSRTLTDGN YLYQVRVIDA 4020
AGNVGATDSQ NVVIDTTAPD PAVKTIAISA ITTDMGLITN DFVTSDTTLA VSGTLGATLS 4080
AGEFAQISLD GGVTWTTLTV VGTSWSYADG HTLTDGTWNY TVRVVDLAGN VGQTATQNVV 4140
VDTTSPEAAK SITITGISDD TGTSSSDFIT SDTTLTVRGV LGAALGANEF AQISTDNGAT 4200
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DSRTLTDGSY VYQVRVLDLA GNTGPVVSKT VVVDTINPTA TPTIVSYTDD VGQRQGTLSS 4380
SQATDDTTPL LNGVLSAPLA SGEVVYLYRN GLLLGAVTMV GALNWTYSDS GLVSGAYTYS 4440
ARVVDLAGNI TSSSDFVLTV DTSIPTTLAQ ITSQTTRDTT PIISGVITAA LASGQYVEVV 4500
INGKTYTSEP GGAVVVDPAH NTWYVQLPDT DALTVSATAY TVTAQVKSSA GNGNNANISN 4560
GTVTVNAAID YTPTWTTASK TTAWGLTYGL DSHGMWTVLA NQQVMQSTDP LTWSKTALTL 4620
YQSGNNYATS SIADYDRNGT GDLFITRDDY GTGYINGFTN NGDGTFSSAI QVTVGTLTWY 4680
GSIVAFDKEG DGYLDFWIGD AGGPDSNTFL WNNAGTLVGN STTSNSGGSA TVGGAVTGYL 4740
SLNEGSGVDL NNDGRIDLVQ HTYNLNNYYT LSSLINQGNG TFVWGQNTTN TFLSGAGSGA 4800

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MSSSVSMTWA DFDGDGDMDL FLPASQGRAN YGSLLFNTNG VLGCPVAVGA TATTYASQFS   4860
LAVDWNHDGL MDIARIAQTG QSYLYTNVSN ASNWTQSALG GSQSGTTSGV AAMDYDWDGA   4920
VDVLVSKQSG SVFLSRNTNT VSYGTSLHLR ITDPNGINVY YGNTVKLYNS AGVLVATQII   4980
NPQSGMGVND TSALVNFYGL NAGETYNAVL IKSTGTTASN IDQTVNTSWG GLQATDATHA   5040
YDLSAEAGTA SNNGKFVGTG YNDTFFATAG TDTYDGSGGW VYSSGTGTWL ANGGMDVVDF   5100
RLSTVGVTAN LSSTAAQATG FNTSTFTNIE GISGSNFNDI LTGSSGDNQL EGRGGNDTLN   5160
IGNGGHDTLL YKLLNASDAT GGNGSDVVNG FTVGTWEGTA DTDRIDIREL LQGSGYTGNG   5220
KASYVNGVAT LDAQAGNIGD FVKVTQSGSD TIVQIDRDGT GGTFATTNVV TLTGVHTDLA   5280
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<212> Type : PRT
<211> Length : 5291
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<213> OrganismName : Escherichia coli O157:H7
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SQPVTFVADK TSALVVLQIS KNEITGNGVD SATLTATVKD QFDNEVNNLP VTFSTASSGL    180
TLTPGESNTN ESGIAQATLA GVAFGEQTVT ASLANNGASD NKTVHFIGDT AAAKIIELTP    240
VPDSIIAGTP QNSSGSVITA TVVDNNGFPV KGVTVNFTSN AATAEMTNGG QAVTNEQGKA    300
TVTYTNTRSS IESGARPDTV EASLENGSST LSTSINVNAD ASTAHLTLLQ ALFDTVSAGD    360
TTNLYIEVKD NYGNGVPQQE VTLSVSPSEG VTPSNNAIYT TNHDGNFYAS FTATKAGVYQ    420
VTATLENGDS MQQTVTYVPN VANAEISLAA SKDPVIANNN DLTTLTATVA DTEGNAIANS    480
EVTFTLPEDV RANFTLGDGG KVVTDTEGKA KVTLKGTKAG AHTVTASMAG GKSEQLVVNF    540
IADTLTAQVN LNVTEDNFIA NNVGMTRLQA TVTDGNGNPL ANEAVTFTLP ADVSASFTLG    600
QGGSAITDIN GKAEVTLSGT KSGTYPVTVS VNNYGVSDTK QVTLIADAGT AKLASLTSVY    660
SFVVSTTEGA TMTASVTDAN GNPVEGIKVN FRGTSVTLSS TSVETDDRGF AEILVTSTEV    720
GLKTVSASLA DKPTEVISRL LNAKADINSA TITSLEIPEG QVMVAQDVAV KAHVNDQFGN    780
PILNESVTFS AEPPEHMTIS QNIVSTDTHG IAEVTMTPER NGSYMVKASL ANGSSYEKDL    840
VVIDQKLTLS ASSPLIGVNS PTGATLTATL TSANGTPVEG QVINFSVTPE GATLSGGKVR    900
TNSSGQAPVV LTSNKVGTYT VTASFHNGVT IQTQTIVKVT GNSSTAHVAS FIADPSTIAA    960
TNSDLSTLKA TVEDGSGNLI EGLTVYFALK SGSATLTSLT AVTDQNGIAT TSVRGAITGS   1020
VTVSAVTTAG GMQTVDITLV AGPADASQSV LKNNRSSLKG DFTDSAELHL VLHDISGNPI   1080
KVSEGLEFVQ SGTNAPYVQV SAIDYSKNFS GEYKATVTGG GEGIATLIPV LNGVHQAGLS   1140
TTIQFTRAED KIMSGTVLVN GANLPTTTFP SQGFTGAYYQ LNNDNFAPGK TAADYEFSSS   1200
ASWVDVDATG KVTFKNVGSK WERITATPKT GGPSYIYEIR VKSWWVNAGD AFMIYSLAEN   1260
FCSSNGYTLP LGDHLNHSRS RGIGSLYSEW GDMGHYTTEA GFHSNMYWSS SPANSNEQYV   1320
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<212> Type : PRT
<211> Length : 1345
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<213> OrganismName : Escherichia coli O157:H7
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LDTVAQTSAF PWGWLAGAAV GGGALGALLA SGGDGDSKTE VINNPTPPAE PGNATPSFLV    180
TDNQGDQRGI LATNDITDDT TPTFSGSGQA GATIQIKDSN GNTIASTQVD NNGHWSVSLP    240
TQSAGEHTWS VVQIVGSTIT DAGSITLTID NSQASVQVAT TAGDNIINAS EQAAGFTLSG    300
TSSHLAQGTE LTVTLNGKTY TTSVGANGAW SVQVPTADAQ ALGEGNQAVL VSGKDATGNT    360
VTGAQLLTVD TQPPTLAINT IAQDNIISAA EHNVALVLSG TSNAEAGQTV TLTVNGKSHT    420
ATVGSDGTWQ VTLPATEVQA LAEGNYAVNA SVSDRAGNTT SHSANFTVDT SAPVVSVNTV    480
AGDDILNNAE QAVAQIISGQ VSGASPGDTV TVKLGTHVLT GIVLADGSWN VALDPAVTRT    540
LDRGANTIFV TVTDAAGNTG AASRAITLVG VSPLITINTV SGDDIISGAE KGAPLTLTGS    600
TQQAETGQTV TVTLAGQSFT TTVQADGSWS LTVPAAAMGN LPDGAVAITA SVTDLSGNTG    660
NTSRTITVDS QAPALSIDPL TADNIINAAE SGQDLPITGT TDAQPGQTVT VTLNGQTYQG    720
VVQPDGTWSV TVPAANVGAL ADGNATVTAS VNDVAGNPSS VSRVALVDAT PPVVTINPVA    780
TDNVINTPEH AQAQIISGTV TGAQAGDIVT VTLNNVDYTT VVDGSGNWSL GVPASVVSGL    840
ADGSYPVSVS VTDKAGNTGS QSLTVTVNTA APLIGINSIA GDDVINASEK GADLQITGTS    900
DQPVNTAITV TLNGQNYTTT TDASGNWSVT VPASAVTALG QANYTVTAAV TSDIGNSATA    960
SHNVLVDSAL PGVTINPVAT DDIINAAEAG VAQTISGQVT GAEDGDTVTI TLGGNTYTAT   1020
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VGSNLTWSVD VPAADIQALG NGDLTVNASV TNQNGNTGSG TRDITIDANL PGLRVDTVAG 1080
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NVEPGQTVTV TFGGKNYTAS VASDGSWTAT VPAADLASLP EGSASALASV SNINGNSASA 1260
VHNYSVDSSA PTIIINTVAS DNIVNASEAD AGVTVSGSTT AEAGQIVTIT LNSPTVQTYQ 1320
ATVQADGSWS INIPAADLEA LTDGSHTLTA TVNDKAGNPA STTHNLAVDL TVPVLTINTI 1380
AGDDIINATE HGQALVISGS STGGEAGDVV TVTLNSKTYT TTLDASGNWS VGVPAADVTA 1440
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<212> Type : PRT
<211> Length : 1461
SequenceName : SEQ ID 283
SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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DSVLTTELFE IGSYGTGSLN ITDKGYVTSS IVAILGYQAN SNGKVVVEKG GEWLIKNNDS 240
SIEFQIGNQG TGEATIREGG LITAENTIIG GNATGVGTLN VQDQDSVITV RRLYNGYFGN 300
GAVNISNNGL INNKEYSLVG VQDGSHGVVN VTDKGHWNFL GTGEAFRYIY IGDAGDGELN 360
VSREGKVDSG IITAGMKETG TGNLTVKDKN SVITNLGTNL GYDGHGEMNI SNEGLVVSNG 420
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DSLWNLKTSS TNAQLLQVGV LGTGELNITT GGIVKARDTQ IALNDKSKGD VRVDGQNSLL 600
ETFNMYVGTS GTGTLTLTNS GTLNVEGGEV YLGVFEPAVG TLNIGAAHGE AAADAGFITN 660
ATKVEFGSGE GVFVFNHTNN SDAGYQVDML ITGDDKDGKV IHDAGHTVFN AGNTYSGKTL 720
VNDGLLTIAS HTADGVTGMG SSEVTIASPG TLDILASTNS AGDYTLTNAL KGDGLMRVQL 780
SSSDKMFGFT HATGTEFAGV AQLKDSTFTL ERDNTAALTH AMLQSDIENT TSVNVGEQSI 840
GGLAMNGGTL IFDTDIPAAT LAEGYISVDT LVVGASDYTW KGRNYQVNGT GDVLIGVPKP 900
WNDPMANNPL TTLNLLEHDD NHVGVQLVKA QTVIGSGGSL TLRDLQGDEV EADKTLHIAQ 960
NGTVVAEGDY GFRLTTAPGD GLYVNYGLKA LNIHGGQKLT LAEHGGAYGA TADMSAKIGG 1020
EGDLAINTVR QVSLSNGQND YQGATYVQMG TLRTDADGAL GNTRELNISN AAIVDLNGST 1080
QTVETFTGQM GSTVLFKEGS LTVNKGGISQ GELTGGGNLN VTGGTLAVEG LNARYNALTS 1140
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<212> Type : PRT
<211> Length : 1343
SequenceName : SEQ ID 284
SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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ANRLTVDVVG QTSAIGINLI GDYTHADLGT GSTIKSNDDG IIIGHSSTLT ATQFTIENSN 180
GIGLTINDYG TSVDLGSGSK IKTDGSTGVY IGGLNGNNAN GAARFTATDL TIDVQGYSAM 240
GINVQKNSVV DLGTNSSIKT SGDNAHGLWS FGQVSANALT VDVTGAAANG VEVRGGTTTI 300
GADSHISSAQ GGGLVTSGSD ATINFSGTAA QRNSIFSGGS YGASAQTATA VINMQNTDIT 360
VDRNGSLALG LWALSGGRIT GDSLAITGAA GARGIYAMTN SQIDLTSDLV IDMSTPDQMA 420
IATQHDDGYA ASRINASGRM LINGSVLSKG GLINLDMHPG SVWTGSSLSD NVNGGKLDVA 480
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<212> Type : PRT
<211> Length : 547
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<213> OrganismName : Escherichia coli O157:H7

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KLNRFESNVA GKMSSGGAAN GSYHSNGLGG HIETGMRFTD GNWNLTPYAS LTGFTADNPE   120
YHLSNGMESK SVDTRSIYRE LGATLSYNMR LGNGMEVEPW LKAAVRKEFV DDNRVKVNSD   180
GNFVNDLSGR RGIYQAGIKA SFSSTLSGHL GVGYSNGAGM ESPWNAVAGV NWSF         234

<212> Type : PRT
<211> Length : 234
      SequenceName : SEQ ID 286
      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKKKVLAIAL VTVFTGMGVA QAADVTAQAV ATWSATAKKD TTSKLVVTPL GSLAFQYAEG    60
IKGFNSQKGL FDVAIEGDST ATAFKLTSRL ITNTLTQLDT SGSTLNVGVD YNGAAVEKTG   120
DTVMIDTANG VLGGNLSPLA NGYNASNRTT AQDGFTFSII SGTTNGTTAV TDYSTLPEGI   180
WSGDVSVQFD ATWTS                                                    195
<212> Type : PRT
<211> Length : 195
      SequenceName : SEQ ID 287
      SequenceDescription :

Sequence
--------
<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MTAESYDDNY LDDEDADWTA TGQGQKSAGD TSFTLAWKPG EEGQKGLIGW FESGDVRAYK    60
IRFPNGTVDV FRGWVSSIGK AVTAKEVITR TVKVTNVGKP SVAEERSKIT PVSAIKVTPT   120
SGTVAKGKTT TLTVSFEPES ATDKTFRAVS ADPSKATISV KDMTITVNGV ATGKVQIPVV   180
SGNGQFAAVA EVTVTEAGAA G                                             201
<212> Type : PRT
<211> Length : 201
      SequenceName : SEQ ID 288
      SequenceDescription :

Sequence
--------
<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MTAESYDDNY LDDEDADWTA TGQGQKSAGD TSFTLAWKPG EEGQKGLIGW FESGDVRAYK    60
IRFPNGTVDV FRGWVSSIGK AVTAKEVITR TVKVTNVGKP SVAEERSKIT PVSAIKVTPT   120
SGTVAKGKTT TLTVSFEPES ATDKTFRAVS ADPSKATISV KDMTITVNGV ATGKVQIPVV   180
SGNGQFAAVA EVTVTEAGAA G                                             201
<212> Type : PRT
<211> Length : 201
      SequenceName : SEQ ID 289
      SequenceDescription :

Sequence
--------
<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MLYNIPCRIY ILSTLSLCIS GIVSTATATS SETKISNEET LVVTTNRSAS NLWESPATIQ    60
VIDQQTLQNS TNASIADNLQ DIPGVEITDN SLAGRKQIRI RGEASSRVLI LIDGQEVTYQ   120
RAGDNYGVGL LIDESALERV EVVKGPYSVL YGSQAIGGIV NFITKKGGDK LASGVVKAVY   180
NSATAGWEES IAVQGSIGGF DYRINGSYSD QGNRDTPDGR LPNTNYRNNS QGVWLGYNSG   240
NHRFGLSLDR YRLATQTYYE DPDGSYEAFS VKIPKLEREK VGVFYDTDVD GDYLKKIHFD   300
AYEQTIQRQF ANEVKTTQPV PSPMIQALTV HNKTDTHDKQ YTQAVTLQSH FSLPANNELV   360
TGAQYKQDRV SQRSGGMTSS KSLTGFINKE TRTRSYYESE QSTVSLFAQN DWQFADHWTW   420
TMGVRQYWLS SKLTRGDGVS YTAGIISDTS LARESASDHE MVTSTSLRYS GFDNLELRAA   480
FAQGYVFPTL SQLFMQTSAG GSVTYGNPDL KAEHSNNFEL GARYNGNQWL IDSAVYYSEA   540
KDYIASLICD GSIVCNGNTN SSRSSYYYYD NIDRAKTWGL EISAEYNGWV FSPYISGNLI   600
RRQYETSTLK TTNTGEPAIN GRIGLKHTLV MGQANIISDV FIRAASSAKD DSNGTETNVP   660
GWATLNFAVN TEFGNEDQYR INLALNNLTD KRYRTAHETI PAAGFNAAIG FVWNF         715
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<212> Type : PRT
<211> Length : 715
SequenceName : SEQ ID 290
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MTKMSRYALI TALAMFLAGC VGQREPAPVE EVKPAPEQPA EPQQPVPTVP SVPTIPQQPG 60
PIEHEDQTAP PAPHIRHYDW NGAMQPMVSK MLGADGVTAG SVLLVDSVNN RTNGSLNAAE 120
ATETLRNALA NNGKFTLVSA QQLSMAKQQL GLSPQDSLGT RSKAIGIARN VGAHYVLYSS 180
ASGNVNAPTL QMQLMLVQTG EIIWSGKGAV SQQ 213
<212> Type : PRT
<211> Length : 213
SequenceName : SEQ ID 291
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MKSKVLALLI PALLGAGAAH AAEVYNKDGN KLDLYGKVDG LHYFSDNSAK DGDQSYARLG 60
FKGETQINDQ LTGYGQWEYN IQANNTESSK NQSWTRLAFA GLKFSDYGSF DYGRNYGLDR 120
YAA 123
<212> Type : PRT
<211> Length : 123
SequenceName : SEQ ID 292
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MATPNPLEPV KGAGTTLWVY NGKGDAYANP LSDDDWQRLA KVKDLTPGEM TAEPYDDNYL 60
DDEDADWTAT GQGQKSAGDT SFTLAWKPGE EGQKGLIGWF ESGDVRAYKI RFPNGTVDVF 120
RGWVSSIGKA VTAKEVITRT VKVTNVGKPS VAEERSEITP ATAIKVTPTS GTVAKGKTTT 180
LTVSFEPESA TDKTFRAVSA DPSKATISVK DMTITVNGVA TGKVQIPVVS GNGQFAAVAE 240
VTVTEAGAAG 250
<212> Type : PRT
<211> Length : 250
SequenceName : SEQ ID 293
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MATPNPLEPV KGAGTTLWVY NGKGDAYANP LSDDDWQRLA KVKDLTPGEM TAEPYDDNYL 60
DDEDADWTAT GQGQKSAGDT SFTLAWKPGE EGQKGLIGWF ESGDVRAYKI RFPNGTVDVF 120
RGWVSSIGKA VTAKEVITRT VKVTNVGKPS VAEERSEITP ATAIKVTPTS GTVAKGKTTT 180
LTVSFEPESA TDKTFRAVSA DPSKATISVK DMTITVNGVA TGKVQIPVVS GNGQFAAVAE 240
VTVTEAGAAG 250
<212> Type : PRT
<211> Length : 250
SequenceName : SEQ ID 294
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
MGWTDMLPEF GGDSYTNADN FMTGRANGVA TYRNTDFFGL VNGLNFAVQY QGNNEGASNG 60
QEGTNNGRDV RHENGDGWGL STTYDLGMGF SAGAAYTSSD RTNDQVNHTA AGGDKADAWT 120
AGLKYDANNI YLATMYSETR NMTPFGDSDY AVANKTQNFE VTAQYQFDFG LRPAVSFLMS 180
KGRDLHAAGG ADNPAGVDDK DLVKYADVGA TYYFNKNMST YVDYKINLLD EDDSFYAANG 240
ISTDDIVALG LVYQF 255

<212> Type : PRT
<211> Length : 255
SequenceName : SEQ ID 295
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MGFIMKLTKT ALCTALFATF TFSANAQTYP DLPVGIKGGT GALIGDTVYV GLGSGGDKFY 60
TLDLKDPSAQ WKEIATFPGG ERNQPVAAAV DGKLYVFGGL QKNEKGELQL VNDAYRYNPS 120
DNTWMKLPTR SPRGLVGSSG ASHGDKVYIL GGSNLSIFNG FFQDTVAAGE DKAKKDEIAA 180
AYFDQRPEDY FFTTELLSYE PSTNKWRNEG RIPFSGRAGA AFTIQGNELV VVNGEIKPGL 240
RTAETHQGKF TAKGVQWKNL PDLPAPKGKS QDGLAGALSG YSNGHYLVTG GANFPGSIKQ 300
FKEGKLHAHK GLSKAWHNEV YTLNNGKWRI VGELPMNIGY GFSVSYNNKV LLIGGETDGG 360
KALTSVKAIS YDGKKLTIE 379
<212> Type : PRT
<211> Length : 379
SequenceName : SEQ ID 296
SequenceDescription :

Sequence

<213> OrganismName : Haemophilus influenzae Rd
<400> PreSequenceString :
MGEQYMLTTI LSFLIVTTVV AYVSWLKTKG DDLKSSKGYF LAGRGLSGLV IGCSMVLTSL 60
STEQLIGVNA VSYKGNFSVI AWTVPTVIPL CFLALYIIGW L 101
<212> Type : PRT
<211> Length : 101
SequenceName : SEQ ID 297
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKNQHKNPLT KALMKTYPYN HFLFFCFILG AFLLGLLSPA YALSIITTKE IDANLLNGAI 60
ESRVVLGKRV FKVEAHGFYF RNNATNSIDI EITSLLRDNQ SFPLTSSAKT SLKIPPNAKI 120
KKSTILVLKG ENAEEVAKIL GVSKEEYQKL ENIAQTKAAN DPMYANTPFS NGSDSSFYDN 180
NPNSPSNNAI NGKDGANGSN GYGANGNDGV NGISGSNGAN GSHSNNNAIG SGIDTDGVLG 240
VDGVNGSSSS SGGSVGGYEN NFTNHGSTNN NTGGYDNFNN GSSSGGSLGN GGLFPIPFGN 300
GDTNNSNNST NTTSPTNGSS SNNATNPSSQ ENNYSSQYCK VPELSPNNTM KLDVIAKDGS 360
CISMNALRDD TKCAYRYDFE AGKAIKQTQY YYVDRENKTQ NIGGCVDLQG AQYAMQLYKD 420
DSKCALQTTS DKGYGMGKTQ TFQTEIVFRG MDNLIHVAVP CSDYARVQDR IVRYEKNDKT 480
QTLTPIVDQY YNDPNNPNKQ EILNRGIATQ LSSQYQEFAC GQWEYNDAKL EAKRPTMLKS 540
YNKLNGEWVE VTPCNFEAGI KSGAVVSPYV MGVPSSKVLS DITTSHYFRI ERKNYGEREQ 600
CQKLYGVNRC QPQYSILILV SPIGAPLTKP LPPKPLNLIY AQPKIMKNTP QPIILSPLKP 660
PSTGLKAF 668
<212> Type : PRT
<211> Length : 668
SequenceName : SEQ ID 298
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MPVIRVLVML ATMMMKLVKT AKEKKVFKNV GISIMGIAFW EAIKDSIKKQ IKKSDWICGN 60
VKTADDYLKT HPNSWFNSAI GVTAITAMLM NVCFADDQSK KEVAQAQKEA ENARDRANKS 120
GIELEQEEQK TEQEKQKTEQ EKQKTEQEKQ KTEQEKQKTE QEKQKTSNIE TNNQIKVEQE 180
QQKTEQEKQK TNNTQKDLVN KAEQNCQENH NQFFIKKLGI KAGIAIEIEA ECKTPKPTKT 240
NQTPIQPKHL PNSKQPHSQR GSKAQELIAY LQKELESLPY SQKAIAKQVD FYRPSSIAYL 300
ELDPRDFNAT EEWQKENLKI RSKAQAKMLE MRSLKPDPQA HLSTSQSLLL VQKIFADVSK 360
EIKVVANTEK KVEKAGYGYS KRM 383
<212> Type : PRT
<211> Length : 383
SequenceName : SEQ ID 299

SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MNYPNLPNSA LEISEQPEVK EITNELLKQL QNALRSNAHF SEQVELSLKC IVRILEVLLS 60
LDFFKNANEI DSSLRNSIEW LTNAGESLKL KMKEYERFFS EFNTSMHANE QEVTNTLNAN 120
AENIKSEIKK LENQLIETTT RLLTSYQIFL NQARDNANNQ ITKNKTQSLE AITQAKNNAN 180
NEISNNQTQA ITNITEAKTN ANNEISNNQT QAITNINEAK ESATTQINAN KQEAINNITQ 240
EKTQATSEIT EAKKTDHYQN IDFFEFE 267
<212> Type : PRT
<211> Length : 267
SequenceName : SEQ ID 300
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKFFSKDLFK KVTPLFLSVY FLSPTLTQAK SRFYVASQYQ VGKMIMKKYN DLKRTIEGAS 60
FSLGWEINPT NYWFYSRYYF FMDYGNVILN KRTGAQANMF TYGFGGDLIM EYNKNPLYVF 120
SLFYGMQVAE NTWTISKHSA NFIIDDWRSI QGFSLKTSNF RMLGLVGFKF QTVLFHHDAS 180
IEVGIKWPFA FEYDSPFVRL FSVFISHTFY L 211
<212> Type : PRT
<211> Length : 211
SequenceName : SEQ ID 301
SequenceDescription :

Sequence

<213> OrganismName : Helicobacter pylori J99
<400> PreSequenceString :
MKKFTLSLFL CCTLLNAEED IFRNNTNETD LTNSFEHGKE NNNLIPAKSD SLESFKEQEN 60
KEKAKQLMDL KALQSVYFSK NRKLQDNNFN VLYVAGNTNK IRLRYAMTTT FIFDNDPIIY 120
VSLGDPSDFE LTYPTNDHYD LSNMLVIKPL LIGVDTNLTV VGASGTIYTL LFV 173

<212> Type : PRT
<211> Length : 173
SequenceName : SEQ ID 302
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MLDYVPWIGN GYRYGNNHRG SNSSTSGVTT QGQSQNASSN EPAPTFSNVG VGLKANVNGT 60
LSGSRTTPNQ QGTPWLTLDQ ANLQLWTGAG WRNDKNGQSD ENYTNFASAK GSTNQQGSTT 120
GGSAGNPDSL KQDKADKSGD SVTVAEATSG DNLTNYTNLP PTSPPHPTDR TRCHSPTRTT 180
PSGCSCSCAA CWAASRCWSI RVGKMITVSL IPPTKNGLTP N 221
<212> Type : PRT
<211> Length : 221
SequenceName : SEQ ID 303
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MDDITAPQTS AGSSSGTSTN TSGSRSFLPT FSNVGVGLKA NVQGTLGGRQ TTTTGNNIPK 60
WATLDQANLQ LWTGAGWRND KTTSGSTGNA NDTKFTSATG SGSGQGSSSG TNTSAGNPDG 120
LQADKVDQNG QVKTSVQEAT SGDNLTNYTN LPPANLTPTA DWPNALSFTN KNNAQRAQLF 180
LRGLLGSIPV LVNKSGQDDN SKFKAEDQKW SYTDLQSDQT KLNLPAYGEV NGLLNPALVE 240
TYFGNTRASG SGSNTTSSPG IGFKIPEQSG TNTTSKAVLI TPGLAWTPQD VGNIVVSGTS 300
FSFQLGGWLV TFTDFIKPRA GYLGLQLTGL DVSEATQREL IWAKRPWAAF RGSWVNRLGR 360
VESVWDFKGV WADQAQLAAQ AATSSTTTTA TGATLPEHPN ALAYQISYTD KDSYKASTQG 420
SGQTNSQNNS PYLHFIKPKK VESTTQLDQG LKNLLDPNQV RTKLRQSFGT DHSTQPQPQS 480

LKTTTPVFGR SSGNLSSVFS GGGAGGGSSG SGQSGVDLSP VERVSGH 527
<212> Type : PRT
<211> Length : 527
SequenceName : SEQ ID 304
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MLKLAVGIFI SPTLTRFSTG FNLAGSVLDQ VLDYVPWIGN GHRYGNNHRG VDDITAPKTG 60
AGSSSGTSTN TSGSRSFLPT FSNVGVGLKA NVQGTLGGSQ TTTTGKDIPK WPTLDPANLQ 120
LWTGAGWRND KASNKQSDEN HTTFKSATGS GQQGGSTTGG SAGNPDSLKQ DKISKSGQNL 180
TTQDGAPQSN STTESASNYD HLPPNLTPTS DWPNALSFTN KNNAQRAQLF LRGLLGSIPV 240
LVNRSGSDDS NKFQATDQKW SYTDLKSDQT KLNLPAYGEV NGLLNPALVE TYFGTTRAGG 300
SGSNTTSSPG IGFKIPEQNN DSKAVLITPG LAWTPQDVGN LVVSGTSLSF QLGGWLVTFT 360
DFVKPRAGYL GLQLTGLDAS DATQRALIWA KRPWAAFRGS WVNRLGRVES VWDLKGVWQD 420
QAQAAAQAAT TAAATGDALP EHPNALAYQI SSTDKDSYKA STQSSGQTNS QNTSPYLHLI 480
KPKKVENTTQ LDQGLKTCWT PTRFAPSCAK ALVQTIPPKP NPNPSKQPHR CLGRIVVTLA 540
VCLVVGVLEE QTAPIRWTSP PLNGWVGGLW GNYPVGVGGI VVRILKVCKT LLFISIFISI 600
FFLNCSLTLF IWTTASLATG LTVVGHFTST TTTLKRQQFS YTRPDEVALR HTNAINPRLT 660
PWTYRNTSFS SLPLTGENPG AWALVRDNTA KGITAGSGSQ QTTYDPTRTE AALTTATTFV 720
LRRYDLAGRC TTSTFRS 737
<212> Type : PRT
<211> Length : 737
SequenceName : SEQ ID 305
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MLDYIPWIGN GHRYGNDHRG SNSSTSGVTT QGQQSQNASG TEPASTFSNV GVGLKANVQG 60
TLGGSQTTTT GKDIPKWPTL DQANLQLWTG AGWRNDKASS GQSDENHTKF TSATGSGQQG 120
SSSGTTNSAG NPDSLKQDKV DKSGDSVTVA ETTSGDNLTN YTNLPPNLTP TADWPNALSF 180
TNKNNAQRAQ LFLRALLGSI PVLVNKSGQD DSNKFQATDQ KWSYTELKSD QTKLNLPAYG 240
EVNGLLNPAL VEVYGLSSTQ GSSTGAGGAG GNTGGDTNTQ TYARPGIGFK LPSTDSESSK 300
ATLITPGLAW TAQDVGNLVV SGTSLSFQLG GWLVTFTDFI KPRSGYLGLQ LTGLDANDSD 360
QRELIWAPPA LNRLSWQLGQ PLGPRGECVG FQGGVGGSSS VRLASSYKYH HRNEGYLIGA 420
HQCFGLSGEL YRPGFVQGFH SKLRPKPKHL PLPALGAGEK SRFLW 465
<212> Type : PRT
<211> Length : 465
SequenceName : SEQ ID 306
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MLGSIPVLVN RSGSDSNKFQ ATDQKWSYTD LQSDQTKLNL SAYGEVNGLL NPALVETYFG 60
TTRTSSTANQ NSTTVPGIGF KIPEQNNDSK ATLITPGLAW TPQDVGNLVV SGTTVSFQLG 120
GWLVTFTDFV KPRAGYLGLQ LSGLNASDSD QRELIWAPRP WAAFRGSWVN RLGRVESVWD 180
LKGVWADQAQ LAAQAATSST TTTATGATLP EHPNALAYQI SYTDKDSYKA STQGSGQTNS 240
QNNSLYLHLI KPKKVESTTQ LDQGLKNLLD PNQVRTKLRQ SFGTDHSTQP QPQSLKTTTP 300
VFGAMSGNLG SVLSGGGAGG AGSTNSVDLS PVERVSGSLT INRNFSY 347
<212> Type : PRT
<211> Length : 347
SequenceName : SEQ ID 307
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MGQQGQSGTS AGNPDSLKQD KISKSGDSLT TQDGNATGQQ EATNYTNLPP NLTPTADWPN 60
ALSFTNKNNA HRAQLFLRGL LGSIPVLVNR SGSDSNKFQA TDQKWSYTDL QSDQTKLNLP 120
AYGEVNGLLN PALVETYFGN TRAGGSGSNT TSSPGIGFKI PEQNNDSKAT LITPGLAWTP 180

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QDVGNLVVSG TSLSFQLGGW LVSFTDFIKP RAGYLGLQLS GLDASDSDQR ELIWAKRPWA    240
AFRGSWVNRL GRVESVWDLK GVWADQAQLA AQAATSEASG SALAPHPNAL AFQVSVVEAS    300
AYSSSTSSSG SGSSSNTSPY LHLIKPKKVE STTQLDQGLK NLLDPNQVRT KLRQSFGTDH    360
STQPQSLKTT TPVFGTSSGN IGSVLSGGGA GGGSSGSGQS GVDLSPVERV SGH            413

<212> Type : PRT
<211> Length : 413
      SequenceName : SEQ ID 308
      SequenceDescription :

Sequence
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<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MGLQLSGLDA SDSDQRELIW AKRPWAAFRG SWVNRLGRVE SVWDLKGVWA DQAHSAVSES     60
QAATSSTTTT ATGDTLPEHP NALAYQISST DKDSYKASTQ GSGQTNSQNT SPYLHLIKPK    120
KVTASDKLDD DLKNLLDPNE VRVKLRQSFG TDHSTQPQPQ PLKTTTPVFG TNSGNLGSVL    180
SGGGTTQDSS TTNQLSPVQR VSGWLVGQLP STSDGNTSST NNLAPNTNTG NEVVGVGDLS    240
KRASIESSRL WIALKP                                                  256
<212> Type : PRT
<211> Length : 256
      SequenceName : SEQ ID 309
      SequenceDescription :

Sequence
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<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MRDNTAKGIT AGSGSQQTTY DPARTEATLT TTTFALRRYD LAGRALYDLD FSKLNPQTPT     60
RDANCQITFN PFGGFGLSGS APQQWNEVKN KVPVEVAQDP TDPYRFAVLL VPRSVVYYEQ    120
LQRGLALPNQ GSSSGSGQQN TTIGAYGLKV KNAEADTAKS NEKLQGDESK SSNGSSSTST    180
TTQRGSTNSD TKVKALKIEV KKKSDSEDNG QLQLEKNDLA NAPIKRGEES GQSVQLKADD    240
FGTAPSSSGS GGNSNPGSPT PWRPWLATEQ IHKDLPKWSA SILILYDAPY ARNRTAIDRV    300
DHLDPKVMTA NYPPSWRMPK WNHHGLWDWK ARDVLFQTTG FDESNTSNTK QGFQKEADSD    360
KSAPIALPFE AYFANIGNLT WFGQALLVFG GNGHVTKSAH TAPLSIWLYI YLVKAVTFRL    420
LLANSLLSKS NIYKKTAN                                                438
<212> Type : PRT
<211> Length : 438
      SequenceName : SEQ ID 310
      SequenceDescription :

Sequence
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<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MRDNIAKGIT AGSNTQQTTY DPTRTEATLT TATTFALRRY DLAGRALYDL DFSKLNPQTP     60
TRDQTGQITF NPFGGFGLSG AAPQQWNEVK DKVPVEVAQD PSNPYRFAVL LVPRSVVYYE    120
QLQRGLALPN QGSSSGSGQQ NTTIGAYGLK VKNAEADTAK SNEKLQGYES KSSNGSSSTS    180
TTQRGGSSNE NKVKALQVAV KKKSGSQGNS GDQGTEQVEL ESNDLANAPI KRGSNNNQQV    240
QLKADDFGTA PSSSGSGTQD GTPTPWTPWL TTEQIHNDPA KFAASILILY DAPYARNRTA    300
IDRVDHLDPK VMTANYPPSW RTPKWNHHGL WDWKARDVLL QTTGFFNPRR HPEWFDGGQT    360
VADNEKTGFD VDNSENTKQG FQKEADSDKS APIALPFEAY FANIGNLTWF EQALLVFGIC    420
LS                                                                 422
<212> Type : PRT
<211> Length : 422
      SequenceName : SEQ ID 311
      SequenceDescription :

Sequence
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<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MLWPFRWVWW KRVLTSQTRA PAKPNPLTVP PTCTWWSLRK LPNPTKLDDD LKNLLDPNEV     60
RARMLKSFGT ENFTQPQPQP QALKTTTPVF GTSSGNLGSV LSGGGYHAGL KHHQSTVTRS    120
TGEWVDR                                                            127
<212> Type : PRT
<211> Length : 127
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SequenceName : SEQ ID 312
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MRDNSAKGIT AGSESQQTTY DPTRTEAALT ASTTFALRRY DLAGRALYDL DFSRLNPQTP 60
TRDQTGQITF NPFGGFGLSG AAPQQWNEVK NKVPVEVAQD PSNPYRFAVL LVPRSVVYYE 120
QLQRGLALPN QGSSSGSGQQ NTTIGAYGLK VKNAEADTAK SNEKLQGDES KSSNGSSSTS 180
TTTQRGGSSG DTKVKALQVA VKKKSGSQGN SGEQGTEQVE LESNDLANAP IKRGEESGQS 240
VQLKAADFGT TPSSSGSGGN SNPGSPTPWR PWLATEQIHK DLPKWSASIL ILYDAPYARN 300
RTAIDRVDHL DPKVMTANYP PSWRTPKWNH HGLWDWKARD VLLQTTGFFN SRRHPEWFDQ 360
GQAVADNTQT GFDTDDTDNK KTRLSKGSWL RQAGPDRPPV WSVLRQHWQP HLVRASAFGV 420
WDLFVLIN 428
<212> Type : PRT
<211> Length : 428
SequenceName : SEQ ID 313
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MFGLKVKNAE ADTAKSNEKL QGAEATGSST TSGSGQSTQR GGSSGDTKVK ALQVAVKKKS 60
GSQGNSGDQG TEQVELESND LANAPIKRGS NPASPTQGSR LRHHPIQFGI WSIRHPHPLK 120
AVACDRANSQ GPPQMIRLDP HSVRCALCL 149
<212> Type : PRT
<211> Length : 149
SequenceName : SEQ ID 314
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MFGLKVKDAT VDSSKQSTES LKGEESSSSS TTSSTSTTQR GGSSGDTKVK ALQVAVKKKS 60
DSEDNGQIEL ETNNLANAPI KRGSNNNQQV QLKADDFGTS PSSSESGQSG TPTPWTPWLA 120
TEQIHKDLPK WSASILILYD APYARNRTAI DRVDHLDPKV MTANYPPSWR TPKWNHHGLW 180
DWKARDVLVQ TTGFFNPRRH PDWFDQGQAV AENTQTGFDT DDTDNKKQGF RKQGEQSPAP 240
IALPFEAYFA NIGNLTWFGQ ALLVFGICLS 270
<212> Type : PRT
<211> Length : 270
SequenceName : SEQ ID 315
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MGSQNQGSTT TTSAGNPDSL VTDKVDQKGQ VQTSGQNLSD TNYTNLSPNF TPTSDWPNAL 60
SFTNKNNAQR AQLFLHGLLG SIPVLVNKSG ENNEKFQATD QKWSYTELKS DQTKLNLPAY 120
GEVNGLLNPA LVETYFGTTR TSSTANQNST TVPGIGFKIP EQNNDSKAVL ITPGLAWTPQ 180
DVGNLVVSGT SFSFQLGGWL VSFTDFVKPR AGYLGLQLTG LDASDATQRA LIWAPPALSG 240
LSWQLGQPVG PRGECVGFEG GVGGSSSVRL ARIYHHRNRG YLTGAPECFG LSGECGGSEC 300
LQAKHELRPN PIH 313
<212> Type : PRT
<211> Length : 313
SequenceName : SEQ ID 316
SequenceDescription :

Sequence

<213> OrganismName : Mycoplasma pneumoniae
<400> PreSequenceString :
MSFGLVGTVN NNGWKSPFRH ETKYRAGYDK FKYYKTHYRG AKKAGTNDDR WRWTAWFDLD 60
FAHQKIVLIE RGELHRQADL KKSDPATNET SKTVWGSIKE KLLQNVNNLH SEKGVFLWFR 120

QSGFTTTRN
<212> Type : PRT
<211> Length : 129
SequenceName : SEQ ID 317
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MAEPLAVDPT GLSAAAAKLA GLVFPQPPAP IAVSGTDSVV AAINETMPSI ESLVSDGLPG 60
VKAALTRTAS NMNAAADVYA KTDQSLGTSL SQYAFGSSGE GLAGVASVGG QPSQATQLLS 120
TPVSQVTTQL GETAAELAPR VVATVPQLVQ LAPHAVQMSQ NASPIAQTIS QTAQQAAQSA 180
QGGSGPMPAQ LASAEKPATE QAEPVHEVTN DDQGDQGDVQ PAEVVAAARD FGAG[illegible]GQQ 240
PGGGVPAQAM DTGAGARPAA SPLAAPVDPS TPAPSTTTTL 280
<212> Type : PRT
<211> Length : 280
SequenceName : SEQ ID 318
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MRYLIATAVL VAVVLVGWPA AGAPPSCAGL GGTVQAGQIC HVHASGPKYM LDMTFPVDYP 60
DQQALTDYIT QNRDGFVNVA QGSPLRDQPY QMDATSEQHS SGQPPQATRS VVLKFFQDLG 120
GAHPSTWYKA FNYNLATSQP ITFDTLFVPG TTPLDSIYPI VQRELARQTG FGAAILPSTG 180
LDPAHYQNFA ITDDSLIFYF AQGELLPSFV GACQAQVPRS AIPPLAI 227
<212> Type : PRT
<211> Length : 227
SequenceName : SEQ ID 319
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MKMVKSIAAG LTAAAAIGAA AAGVTSIMAG GPVVYQMQPV VFGAPLPLDP ASAPDVPTAA 60
QLTSLLNSLA DPNVSFANKG SLVEGGIGGT EARIADHKLK KAAEHGDLPL SFSVTNIQPA 120
AAGSATADVS VSGPKLSSPV TQNVTFVNQG GWMLSRASAM ELLQAAGN 168
<212> Type : PRT
<211> Length : 168
SequenceName : SEQ ID 320
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MTYSPGNPGY PQAQPAGSYG GVTPSFAHAD EGASKLPMYL NIAVAVLGLA AYFASFGPMF 60
TLSTELGGGD GAVSGDTGLP VGVALLAALL AGVALVPKAK SHVTVVAVLG VLGVFLMVSA 120
TFNKPSAYST GWALWVVLAF IVFQAVAAVL ALLVETGAIT APAPRPKFDP YGQYGRYGQY 180
GQYGVQPGGY YGQQGAQQAA GLQSPGPQQS PQPPGYGSQY GGYSSSPSQS GSGYTAQPPA 240
QPPAQSGSQQ SHQGPSTPPT GFPSFSPPPP VSAGTGSQAG SAPVNYSNPS GGEQSSSPGG 300
APV 303
<212> Type : PRT
<211> Length : 303
SequenceName : SEQ ID 321
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MKCPGVSDCV ATVRHDNVFA IAAGLRWSAA VPPLHKGDAV TKLLVGAIAG GMLACAAILG 60
DGIASADTAL IVPGTAPSPY GPLRSLYHFN PAMQPQIGAN YYNPTATRHV VSYPGSFWPV 120
TGLNSPTVGS SVSAGTNNLD AAIRSTDGPI FVAGLSQGTL VLDREQARLA NDPTAPPPGQ 180

LTFIKAGDPN NLLWRAFRPG THVPIIDYTV PAPAESQYDT INIVGQYDIF SDPPNRPGNL 240
LADLNAIAAG GYYGHSATAF SDPARVAPRD [illegible]TNSLGA TTTTYFIRTD QLPLVRALVD 300
MAGLPPQAAG TVDAALRPII DRAYQPGPAP AVNPRDLVQG IRGIPAIAPA IAIPIGSTTG 360
ASAATSTAAA TAAATNALRG ANVGPGANKA LSMVRGLLPK GKKH 404
<212> Type : PRT
<211> Length : 404
SequenceName : SEQ ID 322
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MS[illegible] [illegible]PPFDAIPN PIEDLDVLVA [illegible] GV[illegible]AAQLGEI [illegible]Q 60
KAPHCPAESD QTPAGAAGDG DLPEVGGRVT SPPQPPVAAL TGYSANIGGL SVPHSWNLPP 120
AVRQVAAMFP GATPMYMTGS SDGSYAGLAA AGLAGTGLAG LAARGGSAPT PAAAAPAGAG 180
GAGPAATRPA AQQTPAVPAA AAGSAIPGLP PGLPPGVVAN LAATLAAIPG ATIIVVPPSP 240
NANQ 244
<212> Type : PRT
<211> Length : 244
SequenceName : SEQ ID 323
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MDVALGVAVT DRVARLALVD SAAPGTVIDQ FVLDVAEHPV EVLTETVVGT DRSLAGENHR 60
LVATRLCWPD QAKADELQHA LQDSGVHDVA VISEAQAATA LVGAAHAGSA VLLVGDETAT 120
LSVVGDPDAP PTMVAVAPVA GADATSTVDT LMARLGDQAL APGDVFLVGR SAEHTTVLAD 180
QLRAASTMRV QTPDDPTFAL ARGAAMAAGA ATMAHPALVA DATTSLPRAE AGQSGSEGEQ 240
LAYSQASDYE LLPVDEYEEH DEYGAAADRS APLSRRSLLI GNAVVAFAVI GFASLAVAVA 300
VTIRPTAASK PVEGHQNAQP GKFMPLLPTQ QQAPV[illegible]PPPP DDPTAGFQGG TIPAVQNVVP 360
RPGTSPGVGG TPASPAPEAP AVPGVVPAPV PIPVP[illegible]IPP FPGWQPGMPT IPTAPPTTPV 420
TTSATTPPTT PPTTPVTTPP TTPPTTPVTT PPTTPPTTPV TTPPTTVAPT TVAPTTVAPT 480
TVAPTTVAPA TATPTTVAPQ PTQQPTQQPT QQMPTQQQTV APQTVAPAPQ PPSGGRNGSG 540
GGDLFGGF 548
<212> Type : PRT
<211> Length : 548
SequenceName : SEQ ID 324
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MKNARTTLIA AAIAGTLVTT SPAGIANADD AGLDPNAAAG PDAVGFDPNL PPAPDAAPVD 60
TPPAPEDAGF DPNLPPPLAP DFLSPPAEEA PPVPVAYSVN WDAIAQCESG GNWSINTGNG 120
YYGGLRFTAG TWRANGGSGS AANASREEQI RVAENVLRSQ GIRAWPVCGR RG 172

<212> Type : PRT
<211> Length : 172
SequenceName : SEQ ID 325
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MTRLIPGCTL VGLMLTLLPA PTSAAGSNTA TTLFPVDEVT QLETHTFLDC HPNGSCDFVA 60
GANLRTPDGP TGFPPGLWAR QTTEIRSTNR LAYLDAHATS QFERVMKAGG SDVITTVYFG 120
EGPPDKYQTT GVIDSTNWST GQPMTDVNVI VCTHMQVVYP GVNLTSPSTC AQANFS 176

<212> Type : PRT
<211> Length : 176
SequenceName : SEQ ID 326
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MTPGLLTTAG AGRPRDRCAR IVCTVFIETA VVATMFVALL GLSTISSKAD DIDWDAIAQC 60
ESGGNWAANT GNGLYGGLQI SQATWDSNGG VGSPAAASPQ QQIEVADNIM KTQGPGAWPK 120
CSSCSQGDAP LGSLTHILTF LAAETGGCSG SRDD 154
<212> Type : PRT
<211> Length : 154
SequenceName : SEQ ID 327
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MMQQAVSGIT GALGGAVGGV MGPLTQLPQQ AMQAGQGAMQ PLMSALQQTY GAEGLDVADG 60
ARLVDSIEGE PGLGGEPGAG DVGAGGGGGG TTPTGYLGPP PVPTSSPPTT PAGAPAKSVT 120
PDPVSGTPRA SGPAGMTGMP MVPPGALGAG AEGANKDKPV EKRVTGCAEW STGQGPLNST 180
AECSGEICRR QAGGHQVDAT DPCCAERRQG 210
<212> Type : PRT
<211> Length : 210
SequenceName : SEQ ID 328
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MIRELVTTAA ITGAAIGGAP VAGADPQRYD GDVPGMNYDA SLGAPCSSWE RFIFGRGPSG 60
QAEACHFPPP NQFPPAETGY WVISYPLYGV QQVGAPCPKP QAAAQSPDGL PMLCLGARGW 120
QPGWFTGAGF FPPEP 135
<212> Type : PRT
<211> Length : 135
SequenceName : SEQ ID 329
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MKTTGTTIKL GIVWLVLSVF TVMIIVVFGQ VRFHHTTGYS AVFTHVSGLR AGQFVRAAGV 60
EVGKVAKVTL IDGDKQVLVD FTVDRSLSLD QATTASIRYL NLIGDRYLEL GRGHSGQRLA 120
PGATIPLEHT HPALDLDALL GGFRPLFQTL DPDKVNSIAS SIITVFQGQG ATINDILDQT 180
ASLTATLADR DHAIGEVVNN LNTVLATTVK HQTEFDRTVD KLEVLITGLK NRADPLAAAA 240
AHISSAAGTL ADLLGRIVHC CTAASGTSRA SSSRS 275
<212> Type : PRT
<211> Length : 275
SequenceName : SEQ ID 330
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MTPRSLVRIV GVVVATTLAL VSAPAGGRAA HADPCSDIAV VFARGTHQAS GLGDVGEAFV 60
DSLTSQVGGR SIGVYAVNYP ASDDYRASAS NGSDDASAHI QRTVASCPNT RIVLGGYSQG 120
ATVIDLSTSA MPPAVADHVA AVALFGEPSS GFSSMLWGGG SLPTIGPLYS SKTINLCAPD 180
DPICTGGGNI MAHVSYVQSG MTSQAATFAA NRLDHAG 217
<212> Type : PRT
<211> Length : 217
SequenceName : SEQ ID 331
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MISTTRIDFL WILSVAFASM IALATLLTLI NQVVGTPYIP GGDSPAGTDC SELASWVSNA 60
ATARPVFGDR FNTGNEEAAL AARGFQQGTA PNALVIGWNG HHTAVTLPDG TPVSSGEGGG 120
VRVGGGGAYQ PKFTHHMYLP MDVDAGEDQP PAPDEPVTAV DDVEPEMPAP CPTQRPPVTP 180
RHNLCNKLRT MPGALSAALA AAAPVWPAPI SGCRGFSTSL LAKRNHPVIV GK 232

<212> Type : PRT
<211> Length : 232
SequenceName : SEQ ID 332
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MTTMITLRRR FAVAVAGVAT AAATTVTLAP APANAADVYG AIAYSGNGSW GRSWDYPTRA 60
AAEATAVKSC GYSDCKVLTS FTACGAVAAN DRAYQGGVGP TLAAAMKDAL TKLGGGYIDT 120
WACN 124
<212> Type : PRT
<211> Length : 124
SequenceName : SEQ ID 333
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MAGLNIYVRR WRTALHATVS ALIVAILGLA ITPVASAATA RATLSVTSTW QTGFIARFTI 60
TNSSTAPLTD WKLEFDLPAG ESVLHTWNST VARSGTHYVL SPANWNRIIA PGGSATGGLR 120
GGLTGSYSPP SSCLLNGQYP CT 142
<212> Type : PRT
<211> Length : 142
SequenceName : SEQ ID 334
SequenceDescription :

Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv
<400> PreSequenceString :
MLTRAIKTQL VLLTVLAVIA VVVLGWYFLR IPSLVGIGRY TLYAELPRSG GLYRTANVTY 60
RGITIGKVTG VEPTERGARA TMSIDNGYQI PTDASANVHS VSAVGEQFVD LVSTRTSGPY 120
LRHGQTITTT TVPSQIGPAL DAANRGLAVL PKDRVASVLH EASEAVGGLG SSLNRLIEAT 180
QAIAHDVRGS LEDIDDIIER SAPIIDSQVN SGNEIARWAA NLNTLAAQTA QTDPAVRSIL 240
ANAAPTADQV NATFSDVRES LPQTLANLEV VIDMLKRYHN GVEQALVFLP QSGAIAQSVT 300
TEFPGQAGLG VGGLALNQPP PCLTGFLPAS EWRSPADTST APLPKGTYCR IPMDASNVVR 360
GARNNPCVDV PGKRAATPRE CRSNEAYVPG GTNPWYGDPN QMLSCPAPAA RCDQPVKPGQ 420
VIPAPSVNNG INPLPADQLP GTPPPVNDPL QRPGSGTVQC NGQQPNPCVY TPSTFPTTIY 480
DVQSGKVVAP DGVVYSVEAS THAGADGWKV MLAPTG 516
<212> Type : PRT
<211> Length : 516
SequenceName : SEQ ID 335
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii
<400> PreSequenceString :
MLNNTQFLNL MKSYMKPEFY MSSIKNTTNL DLSSITNTIQ KAMNIFFTTN KISTESMQSL 60
FKKNSEIIQN NINTILNSTK EVINSKDFKQ ATEYHQKCVK SIYETSMDNA KELANIAYEA 120
SNKIFEAANK HITKNIHNAS NNIHNTAEQV QKNFNNKSA 159
<212> Type : PRT
<211> Length : 159
SequenceName : SEQ ID 336
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii
<400> PreSequenceString :
MNIKLVTYFL ILVSSLKVNA DLNHIQDSFK YQEAEQLTIE LPWNDCTAIH KFLEEKLFFS 60
EQQIKKENKI HEKYKQFYLQ HNNKLSDFSM QFLEKKSEIN SVETLISGFL KFCEDNFQTS 120
KSKSHSLNFF QKQQDQWLHN IRNENYKTYY KKKYEDNTFR NIN 163
<212> Type : PRT
<211> Length : 163
SequenceName : SEQ ID 337
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii
<400> PreSequenceString :
MKKLLLIATA SATILSSSVS FAECIDNEWY LRADAGVAMF NKEQDKATGV KLKSNKAIPI 60
DLGIGYYISE NVRADLTLGT TIGGKLKKYG AATNTHFTGT NVSVSHKPTV TRLLINGYVD 120
LTSFDMFDVF VGGGVGPALV KEKISGVSGL ASNTKNKTNV SYKLIFGTSA QIADGVKVEL 180
AYSWINDGKT KTHNVMYKGA SVQTGGMRYQ SHNLTVGVRF GI 222
<212> Type : PRT
<211> Length : 222
SequenceName : SEQ ID 338
SequenceDescription :

Sequence

<213> OrganismName : Rickettsia prowazekii
<400> PreSequenceString :
MKKNMRKQML KIISIIIISL LLSSCSESTR DENGLLTDSQ STIIRDYIIS QNSKNLKVNL 60
KEKFGSNLKG VKLIGIKLTN EDLSGIDFTS CEILRTDFMG SNLEKAILTN SVIQESNFAD 120
SVIKNISGYN ADFQGSIFNN ITLQNTNFVQ SNFSDTAFNK STIINVNFEN SKFSNVLWCH 180
SNIDSSNFQK THLKNNSFKN TNVMNSIFYG ADLGKSVINN TNFTNNYFES SDLSNTKFTS 240
VIIKDSNFTQ SIFNSVNFNN IQSNNSFFSY TSFEDSTLHN IHLTKCDLQN STINSSVFNN 300
FKIDNAILTN MSLNDNTFNN LSIKNSNTNF VRINKSKGFN ITLLNTNYSN AIFSNNDLKE 360
FKVINTDLNN SEIINSNFTN GQFNNVNFSQ SLIQNVNFTD VKITLGNLNQ VALINSNLIN 420
TNIINSVLSN SQINNINYQA YYSFINTNVS NNIVINDNSN QIPPNNIVIN SEKDLQNISN 480
LANMNLTNFN LSNLVFNGVD FSKSIFKKAN LTNTVIKNSI LKDANFSAAI LTKTDFSKSI 540
LTGSIFKFAQ IDQTCFSNSD LTNTDFTEAT IKNTAFDNAN THGIKGLE 588
<212> Type : PRT
<211> Length : 588
SequenceName : SEQ ID 339
SequenceDescription :

Sequence

<213> OrganismName : Porphyromonas gingivalis W83
<400> PreSequenceString :
MIQKFTNVKL NDMRKILSFL MMCSLHLGLQ SQTWHGDPDS VAALPSIGIQ ESSCTRITFE 60
VVFPGFYSVE KREGNQVFQR ISMPGCGSFG NLGEAELPVL KKMIAVPEFS TANVAVKIKE 120
TETFDNYNIY PNPTYVVEEL PEGGTYLVEA FAINNDYYSQ NVSLPSTHYV YSQDGYFRSQ 180
RFIEVTLYPF RYNPVRQEIL FAKKIEVTIT FDNPQPPLQK NTGIFNKVAS SAFINYEADG 240
KSAIENDMVF SRGTTTYISG NVASNLPQNC DYLVIYDDMF NVNQQPHDEI KRLCEHRAFY 300
NGFDVAAVSI KDVLNSFPSN ATSYINETKL KNFIRSVYNQ SNAKRTLDGK LGYVLLIGKP 360
LSKYLADTDN TKVPTSFIHN VSLIPSHPTF GSICASDYFF SCVSPLDTVG DLFIGRFSVT 420
NAHELHNLIE KTINKEISYN PIAHKNILYA EGKGCDAPIL RLFLKEIASG YTVNSILKSN 480
QVSAIDSIFD CLNNGSHHFY FNTHGMPTVW GIGQGLDVNT LTARLNNTSS QGLCTSLSCS 540
SAVADSTIRS LGEVLTTYAP NKGFSAFLGG SRATQYAVYL EGPCPPSEFY EYLPYSLYHN 600
LSTVVGEMLL SSIINTNSVD TYSKFNFNLL GDPALNIMAH GMEVSNCITL PNNTIISSPI 660
TIKNGGCLKI PEKGVLHFTN NGSIQVMSGG TLEIGNQAKI SGETGANPTF ITVYGDGLAI 720
NKQVEIDNID RLNLFSTHSV MPKFHFDSVK FNSAPLYTTN CIVEISNCEF TNRSDIISKN 780
CDLSVENSMF SSSGITVFKP MATSSITGLS TKAKITDNTF FATGNFAYHI TNTPGLTATS 840
NAAIKLDNIP EYYISGNKIV NCDEALVLNN SGNRTNRLHN ITRNVIKNCR IGSTLYNSYG 900
IYNRNKISNN HIGVRLLNNS CFYFDNAPVI NEEDKQTFIS NRTWQLYSSN GTFPLNFHYN 960
SLQGGDTDTW IYNDTYTNRY IDVSNNHWGN NDLFDPNQVF NTPDLFIWIP FWDGLPNGRS 1020
GNSSAEAVEF QTALDCIGNS DYLSAKVALK MMVETYPESD FAIAALKELF RIEKMSGNDY 1080
EGLKDYFRSN PTIISSQNLF PTADFLSARC DIVCENYQSA IDWYENRLNS EISYQDSVFA 1140
VIDLGDIYWN MQLDSLRGTG IDLNILSCEQ RKSLESHQNV KNYLLSTLPE STGTLLPPLE 1200

CNKSSLDKSK IISISPNPAK AVVTIIYYTD NPSCSVIKIY GINGASADIT GLPKHLSEGY 1260
YSIQFNTSNF DPGFYLVTLN VDQKIIDTEK LRIK 1294
<212> Type : PRT
<211> Length : 1294
SequenceName : SEQ ID 340
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MQGKNTIVTT GDYSIGLLSQ TSGNLNTDTI IRVNSDGSVT PSFSDGDDTF IVTAGNHAVG 60
VLACASPGSA CACVSSLDEE STADTGSNEN NAIAKLDMAK GEITTHGTES YAAYANGTVV 120
KAGDTLDYTN ASVTLTDVDI TTHGDNAHAI AARQGTVSFN QGEIYTTGPD AAIAKIYNGG 180
TVTLKNTSAV AHQGSGIVLE SSINGQEATV DILSGSSLRS ANEILYHKDE TSNVTITDSE 240
VSSAADVFIN NIKGHLTVDA TNSKITGSAN ISTDDNTHTY LSLSDNSTWD IKADSTVSNL 300
TVDNSTVYIS RADGRDVEPT RLTITENYVG NNGVLHLRTE LDDDNSATDK VVINGNTSGT 360
TRVKVTNAGG SGAYTLNGIE IISVEGESNG EFIKDSRIFA GAYEYSLTRG NTEATNKNWY 420
LTNFQATSGG ETNSGGSSAP TVAPTPVLRP EAGSYVANLA AANTLFVMRL NDRAGETRYI 480
DPVTEQERSS RLWLRQIGGH NAWRDSNGQL RTTSHRYVSQ LGGDLLTGGF TDSDSWRLGV 540
MAGYARDYNL THSSVSDYRS KGSVRGYSAG LYATWFADDI SKKGAYIDSW AQYSWFKNSV 600
KGDELAYESY SAKGATVSLE AGYGFALNKS FGLEAAKYTW IFQPQAQAIW MGVDHNAHTE 660
ANGSRIENDA NNNIQTRLGF RTFIRTQEKN SGPHGDDFEP FVEMNWIHNS KDFAVSMNGV 720
KVEQDGVSNL GEIKLGVNGN LNPAASVWGN VGVQLGDNGY NDTAVMVGLK YKF 773

<212> Type : PRT
<211> Length : 773
SequenceName : SEQ ID 341
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MTKLKLLALG VLIATSAGVA HAEGKFSLGA GVGVVEHPYK DYDTDVYPVP VINYEGDNFW 60
FRGLGGGYYL WNDATDKLSI TAYWSPLYFK AKDSGDHQMR HLDDRKSTMM AGLSYAHFTQ 120
YGYLRTTLAG DTLDNSNGIV WDMAWLYRYT NGGLTVTPGI GVQWNSENQN EYYYGVSRKE 180
SARSGLRGYN PNDSWSPYLE LSASYNFLGD WSVYGTARYT RLSDEVTDSP MVDKSWTGLI 240
STGITYKF 248
<212> Type : PRT
<211> Length : 248
SequenceName : SEQ ID 342
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKKIALAGLA GMLLVSASVN AMSISGQAGK EYTNIGVGFG TESTGLALSG NWTHNDDDGD 60
VAGVGLGLNL PLGPLMATVG GKGVYTNPNY GDEGYAAAVG GGLQWKIGNS FRLFGEYYYS 120
PDSLSSGIQS YEEANAGARY TIMRPVSIEA GYRYLNLSGK DGNRDNAVAD GLYVGVNASF 180

<212> Type : PRT
<211> Length : 180
SequenceName : SEQ ID 343
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MTTLTARVFT TAEIIYRKTV IALVCHLNCS RQETVTMNKT IMALAIMMAS FAANASVLPE 60
TPVPFKSGTG AIDNDTVYIG LGSAGTAWYK LDTQAKDKKW TALAAFPGGP REQATSAFID 120
GNLYVFGGIG KNSEGLTQVF NDVHKYNPKT NSWVKLMSHA PMGMAGHVTF VHNGKAYVTG 180
GVNQNIFNGY FEDLNEAGKD STAIDKINAH YFDKKAEDYF FNKFLLSFDP STQQWSYAGE 240
SPWYGTAGAA VVNKGDKTWL INGEAKPGLR TDAVFELDFT GNNLKWNKLD PVSSPDGVAG 300
GFAGISNDSL IFAGGAGFKG SRENYQNGKN YAHEGLKKSY STDIHLWHNG KWDKSGELSQ 360

GRAYGVSLPW NNSLLIIGGE TAGGKAVTDS VLISVKDNKV TVQN 404
<212> Type : PRT
<211> Length : 404
SequenceName : SEQ ID 344
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MATGGAALAG KAVMGAAAGA AGGASALQAA FQKASASMET GGDMSSMGSV VSSGGNGGGE 60
AGTAGSSPFA QAAGFGDSGS SSSGGGFAKA AKLATGTASE LAKGVGSQVK QGFQERVSET 120
TGGKLAASIR ESMEPKEASQ SGQFEGNSLG ADSGPDSNEV RS 162
<212> Type : PRT
<211> Length : 162
SequenceName : SEQ ID 345
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKRVLIPGVI LCGADVAQAV DDKNMYMYFF EEMTVYAPVP VPVNGNTHYT SESIERLPTG 60
NGNISDLLRT NPAVRMDSTQ STSLNQGDIR PEKISIHGAS PYQNAYLIDG ISATNNLNPA 120
NESDASSATN ISGMSQGYYL DVSLLDNVTL YDSFVPVEFG RFNGGVIDAK IKRFNADDSK 180
VKLGYRTTRL DWLTSHIDEN NKSAFNQGSS GSTYFSPDFK KNFYTLSFNQ ELADNFGVTA 240
GLSRRQSDIT RADYVSNDGI VAGRAQYKNV IDTALSKFTW FASDRFTHDL TLKYTGSSRD 300
YNTSTFPQSD REMGNKSYGL AWDMDTQLAW AKLRTTVGWD HISDYTRHDH DIWYTELSCT 360
YGDITGRCTR GGLGHISQAV DNYTFKTRLD WQKFAVGDVS HQPYFGAEYI YSDAWTERHN 420
QSESYVINAA GKKTNHTIYH KGKGSLGIDN YTLYMADHIS WRNVSLMPGV RYDYDNYLSN 480
HNISPRFMTE WDIFADQTSM ITAGYNRYYG GNILDMGLRD IRNSWTESVS GNKTLTRYQN 540
LKTPYNDELA MGLQQKIDKN VIARASEAHD QISKSSRTDS ATKTTITEYN NDGKTKTHSF 600
NLSFELAEPL HIRQVDINPQ IVFSYIKSKG NLSLNNGYEE SNTGDNQVVY NGNLVSYDSV 660
PVADFNNPLK ISLNMDFTHQ PSGLVWANTL AWQEARKARI ILGKTNAQYI SEYSDYKQYV 720
DEKLDSSLTW DTRLSWTPQF LKQQNLTISA DILNVLDSKT AVDTTNTGVA TYASGRTFWL 780
DVSMKF 786
<212> Type : PRT
<211> Length : 786
SequenceName : SEQ ID 346
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MKKTLLAIML AGTAFASQAG TLVSQGTEAS ANLTLTKPIV VNNTIQPVKG VYSGTLTAWT 60
PLATGIVGAS DGQSHDYAVT FPDDIYAESS TSADAVISGD NNPDHKLKVS LTTLEQDPPS 120
AASEEIGGKR YMMLKNTGTG GAYRVVSHMK EQVVEPDSYT IRTQAYIYAE 170
<212> Type : PRT
<211> Length : 170
SequenceName : SEQ ID 347
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MGIYHWSRKT KMKRTKSIRH ASFRKNWSAR HLTPVALAVA TVFMLAGCEK SDETVSLYQN 60
ADDCSAANPG KSAECTTAYN NALKEAERTA PKYATREDCV AEFGEGQCQQ APAQAGMAPE 120
NQAQAQQSSG SFWMPLMAGY MMGRLMGGGA GFAQQPLFSS KNPASPAYGK YTDATGKNYG 180
AAQPGRTMTV PKTAMAPKPA TTTTVTRGGF GESVAKQSTM QRSATGTSSR SMGG 234

<212> Type : PRT
<211> Length : 234
SequenceName : SEQ ID 348
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MTKMSRYALI TALAMFLAGC VGQREPAPVE EVKPAPEQPA EPQQPVPTVP SVPTIPQQPG 60
PIEHEDRTAP PAPHIRHYDW NGAMQPMVSK MLGADGVTAG SVLLVDSVNN RTNGSLNAAE 120
ATETLRNALA NNGKFTLVSA QQLSMAKQQL GLSPQDSLGT RSKAIGIARN VGAHYVLYSC 180
ASGNVNAPTL QMQLMLVQTG EIIWSGKGAV SQQ 213
<212> Type : PRT
<211> Length : 213
SequenceName : SEQ ID 349
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MTKLMQFVQR CYYMTNKKMY FILILVFTLL QVCFFALWKA RDGSTTSLEC TSTLTRNAKT 60
DHSLYYSANL SVILKKDGSG SFTIVGLTDE DTPRKFSHSY FFTYKIDSNG RISGNAKAKV 120
SGLENQIKDE NFRLNFLDAS LTGKGNARLS KFNNVYIFSI PGLIINTCAP I 171

<212> Type : PRT
<211> Length : 171
SequenceName : SEQ ID 350
SequenceDescription :

Sequence

<213> OrganismName : Shigella flexneri 2a str. 2457T
<400> PreSequenceString :
MGRISSGGMM FKAITTVAAL VIATSAMAQD DLTISSLAKG ETTKAAFNQM VQGHKLPAWV 60
MKGGTYTPAQ TVTLGDETYQ VMSACKPHDC GSQRIAVMWS EKSNQMTGLF SAIDEKTSQE 120
KLTWLNVNDA LSIDGKTVLF AALTGSLENH PDGFNFK 157
<212> Type : PRT
<211> Length : 157
SequenceName : SEQ ID 351
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKQFLEKAV FTVAATAATV VLGNKMADAD TYTLQEGDSF FSVAQRYHMD AYELASMNGK 60
DITSLILPGQ TLTVNGSAAP DNQAAAPTDT TQATTETNDA NANTYPVGQC TWGVKAVATW 120
AGDWWGNGGD WASSASAQGY TVGNTPAVGS IMCWTDGGYG HVAYVTAVGE DGKVQVLESN 180
YKDQQWVDNY RGWFDPNNSG TPGSVSYIYP N 211
<212> Type : PRT
<211> Length : 211
SequenceName : SEQ ID 352
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MSIKNILENK TTTIKVSFAG IATAASLILP MAVQAETTYT VKSGDTLSEI ASTHGTTVDK 60
LAKLNKINNI HLIHAGQILE LDAATEDTDA TPVQESQINE AETSASAKTS QTSEVTTTAP 120
VQESQTSEVI TSAPAETSQT SEVPTEANQT NEVSSAVSVE TSQTSEATTS APVETSQTSE 180
ATTAEPTETK TSQTNEVAAS AEENQTTSNT SGLSTSDAAA KEFIAQKESG GNYNAKNGQY 240
YGRYQLSDSY LNGDLSEENQ ERVADAYVSS RYGSWTAAQA FWNANGWY 288
<212> Type : PRT
<211> Length : 288
SequenceName : SEQ ID 353
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKCQAFEDFK ATSLNKLSYT TGGATDGEII ANRMLQGKAT KGEITMYTWN IIQNGWVNSL 60
VSWGIGGYNS SIGYSAQGNR GFSNYPYDVS MDSDNSSSSS NTTGGYVNYN QSFNSGW 117

<212> Type : PRT
<211> Length : 117
SequenceName : SEQ ID 354
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MRYSQICRKS LALLATGMIL TTSTLPSISI LAEDSTGAPA RPDGQAPAGG GANTTTYDYS 60
GINSGVLVAN GSKVTSSSKT KSTTSAQNTA LVQNGGSLTL HKANLIKSGD DNNGDNDNFY 120
GINSILLAVN ERSKAYVSNS KLKASSSGSN GIFATDKATI YANKTSIATT ADNSRGLDAT 180
YNGNIIANKM AISTKGAHSA AIATDRGGGN ISTTNSSLNT SGSGSPLLYS TGNIQVNHVT 240
GTSSNSQIAG MEGLNTILIH NSNLISTMTN KTASDPIANG VIIYQSQSGD AEATTGQSAH 300
FELSKSKLTS SITSGSMFYL TNTSANIILN QSTLNFDANK AKLLTVAGNS ANNWGTPGSN 360
GATVNFTGHK QTLKGDVDVD SISTLNMYLL DKTNYTGKTA VSTNSTNISP STSPITMNIS 420
KNSKWVLTGH STVTNLNAEK GAKIVDKDGK TVSVISSSGQ KLVKGKSKYS LTVTGTYSQK 480
VTTSSSNKPS SSYINRSDFD NYFKTTTAFV NNTKNTSN 518
<212> Type : PRT
<211> Length : 518
SequenceName : SEQ ID 355
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MNKIGDTLRD ARIEKKLSFD DVVDKTGIAP HYILAMELDQ LKLLPEGKTN EYLEKYAHAV 60
GLDPVSIIHG YRNQEMSDEL ILPSSAELAA SSDSNIEKKN EGKSIEEPQE LAIDSLDVTQ 120
NITEETPQIE DFKVESEEAS KKIEKIPSRL SKYDYDEEPK KKFPWALILL ILLALTIISY 180
VGYVVYNQLQ TDSNKTELST STKKSKDTKN DANSTTQSQT SITTDFADGG NNITLSNTNG 240
KVEVTFTLTG DEESWVSATN TTDGESGTTL TATDKTYTVT LAEGSTTSML TVGSPSGVEI 300
TINGQKVDTT NLVNAGLTNI NLTVQ 325
<212> Type : PRT
<211> Length : 325
SequenceName : SEQ ID 356
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKSRKRQRKG LVRKNEIIIL TLFVASAVSL LAFTNSFGVL AKSLHLEKIN KSITISLPFG 60
KKKMEQTARY YSGEQVQISS SAKKDSLGKG LSHYQNWIGT VKKIKSQKDS RQKHHYSYEV 120
TFDNGKALKY VQEKDLVKTK RSKYSKGQIV KLKSSATADL DGSSLTDYRA SAGKIDHISY 180
NHSNTTGGYK YDITFDEGGK VTNIQEKDLD KVYEVQLKSE NTAAQNNEIL KQAFAYAKQH 240
SGTILSLPNG EFKIGSQTPD KDYITLTSDT EIRGDNTTLL VEGSAYWFAF ATGTSASDGV 300
KNFTMRNINI KASDLEKGNQ FMIMADHGDN WKICNNSFTM VHKKGSHIFD LGSLQNSAFE 360
GNQFTGYAPE LTNVSKIDDN ADLHDFYSEV IQLDAAESSG VWDGGLIKAI DPNYENYNKE 420
KQLCNNITIA NNSFVPYIDS HGKIIAYSGT IGQHSSDVGL VKIYDNVFSN SLVSRFNQNG 480
KSEAWIFKAI HLKSNYNNAV YANSIS 506
<212> Type : PRT
<211> Length : 506
SequenceName : SEQ ID 357
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MRKLKVALFA SSILGMLAVS SYTAADTEDN QVTISHYNEQ AGTFDVNAVQ AANGKTIQSI 60
DVAIWSEENG QDDLKWYHAS NDGSNQLTVH FNAENHGSKV GSYIAHAYIT YTDGNRVGVN 120

LGKRKLSLSA PQLSLKQGGL QLFSKLKPSA ADQLFSAVWS DENGQDDLHW YTADADGNTL 180
AGYANHKGYG TYHVHTYLKQ NGKMIPISAQ DIDIPKPKVK IQIDKINDTS YDVVVNNVPP 240
YISSVAIPVW SEQNGQDDLK WYQATKVADG IFKTTVYLKT HRFELGNYQA HIYGDSQLSK 300
KLDGLGETHF NVPSIINYED PQVTIDHYNI NKGTFDVTVA ETDNSKAIQS ISAAVWSDAN 360
QANLYWYEAK QLANGKAAIT VDVQKHGNQT GSYNVHVYVH YNDGTTSGHV LANQQLNQIV 420
HYQPSAVRIT AYMNEKNTYP VGQCTWGVKE LAPWIPNWLG NGGQWASTVA VKGFKIGTVP 480
KVGAIACWSD GGYGHVAYVT HVESNNRIQV KEANYKNQQY ISNFRGWFDP TTSYLGRLTY 540
IYPD 544
<212> Type : PRT
<211> Length : 544
SequenceName : SEQ ID 358
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MANNYSRRQQ PTKKTKGTSR KRPTEHIKTG FSALQKSVAI IAGILGIITA LITINNYRNS 60
SHNDKKDSTS KTTIIKEKEV DDSNSNNNAA NSQAENDSNN NNNSAESNQN QTATTANDSN 120
SNSANQNQAN SQSQANNQQN QNNANAGQ 148
<212> Type : PRT
<211> Length : 148
SequenceName : SEQ ID 359
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKIFSFGTIR NNTALKPNYD DTTAFSGFGT IRNNTALKQS TNCASWFNRF GTIRNNTALK 60
LTILINGVSF CFGTIRNNTA LKPRGPIFVS TFRNRAIHLS QISASK 106
<212> Type : PRT
<211> Length : 106
SequenceName : SEQ ID 360
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKRKRNLYFL IGLFLTVFLL IGCSMQKKTK SESSSTSQKT TLQTKQSSEK STDAKQTTEA 60
HSESSQSSSH SNNEETLAPI DTGAVLKADY SSMAGTWKNE EGQTLTFDQR GLTTPGMTVS 120
LLNIDQDGNL LLNVETGTKK NLTLYIVPAN KTLSNQYFSN GQSDESDKTK DRIVSSESLN 180
SGKFTNRVYY HVSTH 195
<212> Type : PRT
<211> Length : 195
SequenceName : SEQ ID 361
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MTPKKIKIAL TALISLMLAL FLFLFNHHSV RENSQQEKLK ISKASSKKSQ TSTSSVMTSS 60
RKATEQTSQA QTQSQSQAEQ SNPNVILPIP QELVGTYKGS SPQASEITFT ISSNGQLRAQ 120
ANFDPASDIN DVTATVSGVR KVGADTYIWE FVSGSSAALL PGVTGIGGLG KMQPGFILKG 180
GQLTPIMFTG SVDGEIDYSH PNPYPVSLNK Q 211
<212> Type : PRT
<211> Length : 211
SequenceName : SEQ ID 362
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKIINVIVL SLSVFFLIAC SNSSTGEKTS QSSEETKVRL IVKTDSNKTD EKVAFKKGAT 60

VMDVLKDNYK VKESGGFITT IDGVTQDKKA GRYWMFDVND KLASKAADKI KVKNGDKIEF 120
YLKVYKGKN 129
<212> Type : PRT
<211> Length : 129
SequenceName : SEQ ID 363
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MSNKPWEEKV TDATTDNEEM TRNSKDASII STPILTILLS LFFLIIIGIL FFVLYTSNGG 60
SNEKAATSGF YSSSKTVKKA KNEANSQTDE QTTEAETSSS ETTSSSSDSD GETITVQGGE 120
GAAAIAARAG ISVDKLYELN PEHMTHGYWY ANPGDNIKIK 160
<212> Type : PRT
<211> Length : 160
SequenceName : SEQ ID 364
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MPDNRMNYSI DSNMQFPLVE ITLETGEFAY IQRGSMVYHT PSVTLNTKVN GRGSGLGKLV 60
GAIGRSVTSG ESFFITQAVS NASDGKLALA PSMPGQVIAL ELGEKQYRLN DGAFLALDGS 120
AQYQMKAQSV GRALFGGQGG LFVMTTEGQG TLLANSFGSI KKIELQNQEI TIDNAHVVAW 180
SRDLNYDIHL ENGFMQSIGT GEGVVNTFRG TGEIYVQSLN LQQFAGVLQG FITNTNR 237

<212> Type : PRT
<211> Length : 237
SequenceName : SEQ ID 365
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus mutans UA159
<400> PreSequenceString :
MKKNYFWYGL LGLLALYLIT IAFIPGFHIF FSNMLMLALF FMLIALSNRS IFFFFLALGF 60
LSIYLKDIFH FDYSTGPLFT GIIIIGVILN SFLKPHYSYS YKGNHYFNMK QHANYIDNET 120
DVFLKTLFSE NTSYVTSQEL NKIIIDTKFG EQSVDLSQAQ FMTDSPEIHI DVSFGETNLR 180
IPNNWKIINK THSPFASISF SGFPSTNGDF INVTLTGTVA MGSLNIQY 228
<212> Type : PRT
<211> Length : 228
SequenceName : SEQ ID 366
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKSITKKIKA TLAGVAALFA VFAPSFVSAQ ESSTYTVKEG DTLSEIAETH NTTVEKLAEN 60
NHIDNIHLIY VDQELVIDGP VAPVATPAPA TYAAPAAQDE TVSAPVAETP VVSETVVSTV 120
SGSEAEAKEW IAQKESGGSY TATNGRYIGR YGSWTAAKNF WLNNGWY 167
<212> Type : PRT
<211> Length : 167
SequenceName : SEQ ID 367
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKHSHKKSFD WYSMQQRYSI RKYYFGAASV LLGTALVLGA AASVQTVQAE ENKQETTNSI 60
SVGRGEAATK PAEVSASNKE KTYAAPTVAN PVETTPVKTE EVTKPAEKVE EAKDKKEEVT 120
HQDAVDKSKL LTALSRAKKL ESKLYTEASA ANLQTSIQAG QSLLGKADAT EAELSAAESS 180
IQSFIIGLEL RSNSNKETVS ETPVAKKADA VESKEGAKPA ATTERSAVDS AILPTSTADK 240
VETTSAPASI NEILKLGLSL SDARQNPAIR KEDVNRGYSG FRAASNPANP IVSGSGNTVA 300

FADISQGGRS YSFRGYGNSR GGNSIHYDVT TVRSGNSVNF TISYSAPGDS REFVNNNFIL 360
DKGDGFGNPS NATITSSNPR VREQSKSISQ GANYVSHSGY SMTSAISTNT EQTIRFSLPI 420
INLNGDLSVR LKPVTFNVDQ GGGGAATSND PYSNSNYYYR ANPLYLDANP YGGTNNKTVS 480
EDIDFQTVYL PTSKLPEGQT RLVREGEKGQ RQITYKVHRF GNETLLGLPI SNSVTKEAKP 540
RIMQIGVAKD LIDTVKPRVD QNKVGDTNNL TFYLDNDGNG VYTEGVDELV QKIAIKDGAK 600
GEKGDQGERG LTGAKGEKGD RGERGLTGAQ GAKGEKGDRG ERGLTGAQGA KGEKGDRGER 660
GLTGAQGAKG EKGDRGERGL TGAQGAKGEK GAQGERGLTG AQGAKGEKGD QGERGLTGAQ 720
GAKGEKGDQG ERGLTGAQGA KGEKGAQGER GLTGTQGAKG EKGDRGERGL TGAQGAKGEK 780
GDRGERGLTG AQGAKGEKGA QGERGLTGAQ GAKGEKGDQG ERGLTGAQGE KGDRGERGLT 840
GAKGEKGDQG ERGITGAKGE KGAQGERGLT GAQGAKGEKG DQGERGLTGA QGEKGAQGQA 900
GRDGVTPTVT VKDNKNDGTH TITINDGRGN VTSTVVRDGF DGASPLVATQ RNDADKTTTV 960
IFYYDKNGNN ELDASDKKLK EVVIADGAKG EKGDKGEQGL QGRDGEQGPK GEDGKTPTVK 1020
VTDGQDGTHT ITINDGKGGI TTTVVRDGFD GASPLVSTHR NEADKTTTVI FYYDLNDNNQ 1080
FDEGDTKLKE VVIADGKQGP KGDKGDNGKD GETPEVTVTD NNNGTHTITI TQPDNRPSLT 1140
TIVKNGEDGK TPKVKAERDD AKKQTTLTFY IDKDGDGSYT AGKDELVQTT VVKDGQDGAA 1200
GASGRDGKEV LNGKVDPTTE GKDGDTFVNT QTGDVFVKKG NTWEPAGNIK GPKGDKGADG 1260
AKGEKGAQGE RGLTGAQGVK GEKGDQGERG LTGSKGEKGD QGERGLTGAQ GAKGDKGEQG 1320
LQGRDGAQGP KGADGQRGPA GPQGPKGEQG NPGTPGKDGK SLIAVKNGVL VTITPVEGRP 1380
QTTFVEDGQK GADGKTPTVT ITEGQNGTHT LTVHNPGSPD VTTTIRDGAT GQAGRDGKDV 1440
LNGKVNPQPN QGKNGDKYIN IETGDVYVKN NGNWDKEGNI KGPKGDKGAD GAKGEKGDQG 1500
ERGLTGAQGA KGADGAVGRD GRDGKDVLNG KANPEAHQGK DGDKYVNTET GDVFVKNNGN 1560
WDKEGNIKGP KGDKGADGAK GEKGDRGERG LTGAQGAKGA DGAAGRDGRD GRDGKDVLNG 1620
KVNPEANQGK DGDKYVNTET GDVFVKNNGN WDKEGNIKGS KGDKGERGED GKTPEVTVTP 1680
GKDGHSTDIT FTVPGKDPVT VNVKDGENGL NGKTPKVDLL RVQGKNGNPS HTIVTFYTDE 1740
NNDGKYTPGT DELLGSEMIK DGAKGADGRD GKSLLTVKDG KETKVYQEDP ANPGQPLNPE 1800
KPLAVIRDGV DGKSPTVTAV RKDEAGHKGV EITVDNHDGS QPTTVFVQDG AKGKTGATGQ 1860
DGQTPTITTQ RGQDGQSTVV TITTSGKDPV TFTVKDGKNG KDGRAPKIKV EDITSPSRIR 1920
RDTDAAATPT RNGIRVTVYD DVNDNGVYDE GVDKVLNSKD IYNGIDGRDG SAPTITTKDN 1980
GDGTHTITVQ NPDGSESTTV VKDGKDGKTA NITTTENPDG SHTITVTNPD GSTKETVVKN 2040
GKDGKTPKVE VTDNNDGTHT VKVTDGDGNV TNAIIKDGKD GKAATATTTE NPDGSHTVTI 2100
TNPDGTKNEF VVKNGRDGVD GRTPTASVRD NGDGSHTIVI TNPEGVTTET TVRDGKSPKV 2160
TITDEQNGTH KISVLNGDGT TTETIIKDGK SPVATVRDNQ DGTYTIRVEN GNGTVSETTV 2220
RDGKSPTAKV VDNGDGTHTI TVVNSDGITT TTTVRDGREP KLEVIDNNDG SHTIKVTGAD 2280
GKGTTTTIFD GKSPKANIVD NGDGTHTLTI VDSDGREYKS IIKDGKDGKD SVSPTVTVKN 2340
NNDGTHVVTI TNPDGSKTEM VIKDGKDGKS PKVSVEDNGD GSHTITIINS DGTVTKTVIK 2400
DGKDGRDGRD GRDGKDGKDG KCGCQDKPVT PSNDKPVPPT PNVPTPEVPV KPVPAQPTPN 2460
VPTPEVPVQP TPAVSTPEVP VKPVPAVPEQ PVVPTPAQPA TPVNANPVAP TTGKENRGDK 2520
LPETGSQSDY ISVLLGSGIL LSLYVGRRKE D 2551
<212> Type : PRT
<211> Length : 2551
SequenceName : SEQ ID 368
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKKRMLLAST VALSFAPVLA TQAEEVLWTA RSVEQIQNDL TKTDNKTSYT VQYGDTLSTI 60
AEALGVDVTV LANLNKITNM DLIFPETVLT TTVNEAEEVT EVEIQTPQAD SSEEVTTATA 120
DLTTNQVTVD DQTVQVADLS QPIAEAPKEV ASSSEVTKTV IASEEVAPST GTSVPEEQTA 180
ETSSAVAEEA PQETTPAEKQ ETQTSPQAAS AVEATTTSSE AKEVASSNGA TAAVSTYQPE 240
ETKIISTTYE APAAPDYAGL AVAKSENAGL QPQTAAFKEE IANLFGITSF SGYRPGDSGD 300
HGKGLAIDFM VPERSELGDK IAEYAIQNMA SRGISYIIWK QRFYAPFDSK YGPANTWNPM 360
PDRGSVTENH YDHVHVSMNG 380
<212> Type : PRT
<211> Length : 380
SequenceName : SEQ ID 369
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MTILGKDTVQ QSAKGESVTQ EATPEYKLEN TPGGDKGGNT GSSDANANEG GGSQAGGSAH 60
TGSQNSAQSQ ASKQLATEKE SAKNAIEKAA KNKQDEIKGA PLSDKEKAEL LARVEAEKQA 120
ALKEIENAKT MEDVKEAETI GVQAIAMVTV PKRPVAPNAA PKTTSAPQAT AGTMQDVTYQ 180
SPAGKQLPNT GSASSAALAS LGLVVATSGF ALLGRKTRRR K 221

<212> Type : PRT
<211> Length : 221
SequenceName : SEQ ID 370
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MMTTGCSMGA YHALNFFLQH PDVFTKVIAL SGVYDARFFV GDYYNDDAIY QNSPVDYIWN 60
QNDGWFIDRY RQAEIVLCTG LGAWEQDGLP SFYKLKEAFD KKQIPAWFAE WGHDVAHDWE 120
WWRKQMPYFL GNLYL 135
<212> Type : PRT
<211> Length : 135
SequenceName : SEQ ID 371
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MNKGLFEKRC KYSIRKFSLG VASVMIGATF FGTSPVLADS VQSGSTANLP ADLATALATA 60
KENDGHDFEA PKVGEDQGSP EVTDGPKTEE ELLALEKEKP AEEKPKEDKP AAAKPETPKT 120
VTPEWQTVEK KEQQGTVTIR EEKGVRYNQL SSTAQNDNAG KPALFEKKGL TVDANGNATV 180
DLTFKDDSEK GKSRFGVFLK FKDTKNNVFV GYDKDGWFWE YKSPTTSTWY RGSRVAAPET 240
GSTNRLSITL KSDGQLNASN NDVNLFDTVT LPAAVNDHLK NEKKILLKAG SYDDERTVVS 300
VKTDNQEGVK TEDTPAEKET GPEVDDSKVT YDTIQSKVLK AVIDQAFPRV KEYSLNGHTL 360
PGQVQQFNQV FINNHRITPE VTYKKINETT AEYLMKLRDD AHLINAEMTV RLQVVDNQLH 420
FDVTKIVNHN QVTPGQKIDD ERKLLSSISF LGNALVSVSS DQTGAKFDGA TMSNNTHVSG 480
DDHIDVTNPM KDLAKGYMYG FVSTDKLAAG VWSNSQNSYG GGSNDWTRLT AYKETVGNAN 540
YVGIHSSEWQ WEKAYKGIVF PEYTKELPSA KVVITEDANA DKKVDWQDGA IAYRSIMNNP 600
QGWKKVKDIT AYRIAMNFGS QAQNPFLMTL DGIKKINLHT DGLGQGVLLK GYGSEGHDSG 660
HLNYADIGKR IGGVEDFKTL IEKAKKYGAH LGIHVNASET YPESKYFNEK ILRKNPDGSY 720
SYGWNWLDQG INIDAAYDLA HGRLARWEDL KKKLGDGLDF IYVDVWGNGQ SGDNGAWATH 780
VLAKEINKQG WRFAIEWGHG GEYDSTFHHW AADLTYGGYT NKGINSAITR FIRNHQKDAW 840
VGDYRSYGGA ANYPLLGGYS MKDFEGWQGR SDYNGYVTNL FAHDVMTKYF QHFTVSKWEN 900
GTPVTMTDNG STYKWTPEMR VELVDADNNK VVVTRKSNDV NSPQYRERTV TLNGRVIQDG 960
SAYLTPWNWD ANGKKLSTDK EKMYYFNTQA GATTWTLPSD WAKSKVYLYK LTDQGKTEEQ 1020
ELTVKDGKIT LDLLANQPYV LYRSKQTNPE MSWSEGMHIY DQGFNSGTLK HWTISGDASK 1080
AEIVKSQGAN DMLRIQGNKE KVSLTQKLTG LKPNTKYAVY VGVDNRSNAK ASITVNTGEK 1140
EVTTYTNKSL ALNYVKAYAH NTRRNNATVD DTSYFQNMYA FFTTGSDVSN VTLTLSREAG 1200
DEATYFDEIR TFENNSSMYG DKHDTGKGTF KQDFENVAQG IFPFVVGGVE GVEDNRTHLS 1260
EKHDPYTQRG WNGKKVDDVI EGNWSLKTNG LVSRRNLVYQ TIPQNFRFEA GKTYRVTFEY 1320
EAGSDNTYAF VVGKGEFQSG RRGTQASNLE MHELPNTWTD SKKAKKATFL VTGAETGDTW 1380
VGIYSTGNAS NTRGDSGGNA NFRGYNDFMM DNLQIEEITL TGKMLTENAL KNYLPTVAMT 1440
NYTKESMDAL KEAVFNLSQA DDDISVEEAR AEIAKIEALK NALVQKKTAL VADDFASLTA 1500
PAQAQEGLAN AFDGNLSSLW HTSWGGGDVG KPATMVLKEA TEITGLRYVP RGSGSNGNLR 1560
DVKLVVTDES GKEHTFTATD WPDNNKPKDI DFGKTIKAKK IVLTGTKTYG DGGDKYQSAA 1620
ELIFTRPQVA ETPLDLSGYE AALAKAQKLT DKDNQEEVAS VQASMKYATD NHLLTERMVE 1680
YFADYLNQLK DSATKPDAPT VEKPEFKLSS VASDQGKTPD YKQEIARPET PEQILPATGE 1740
SQFDTALFLA SVSLALSALF VVKTKKD 1767
<212> Type : PRT
<211> Length : 1767
SequenceName : SEQ ID 372
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pneumoniae R6
<400> PreSequenceString :
MKLYNKSELR YSRIFFDKRP PAFAFILIIS TAIILSGALV GAAYIPKNYI VKANGNSVIT 60
GTEFLSAISS GKVVTLHKSE GDMVNAGDVI ISLSSGQEGL QASSLNKQLV KLRAKEAIFQ 120
KFEQSLNEKY NRMSNSGEEQ EYYGKVEYYL SQLNSENYNN GTQYSKIQDE YTKLNKITAE 180
RNQLDADLQT LQNELIQLQQ QGDSPSLSDT TSADDKAKLE TKILEITTKI EALKTNITSK 240
NSEIDSQQSN IKDMNRTYND PTSQAYNIYA QLVSELGTAR SNNNKSITEL EANLGVATGQ 300
DKAHSILAPN EGTLHYLVPL KQGMSIQQGQ TIAEVSGKEK GYYVEAFVLA SDISRVSKGA 360
KVDVAITGVN SQKYGTLKGQ VRQIDSGTIS QETKEGNISL YKVMIELETL TLKHGSETVV 420

LQKDMPVEVR IVYDKETYLD WILEMLSFKQ 450
<212> Type : PRT
<211> Length : 450
SequenceName : SEQ ID 373
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MNKGLHRIIF SKKHSTMVAV AETANSQGKG KQAGSSVSVS LKTSGDLCGK LKTTLKTLVC 60
SLVSLSMVLP AHAQITTDKS APKNQQVVIL KTNTGAPLVN IQTPNGRGLS HNRYTQFDVD 120
NKGAVLNNDR NNNPFLVKGS AQLILNEVRG TASKLNGIVT VGGQKADVII ANPNGITVNG 180
GGFKNVGRGI LTIGAPQIGK DGALTGFDVR QGTLTVGAAG WNDKGGADYT GVLARAVALQ 240
GKLQGKNLAV STGPQKVDYA SGEISAGTAA GTKPTIALDT AALGGMYADS ITLIANEKGV 300
GVKNAGTLEA AKQLIVTSSG RIENSGRIAT TADGTEASPT YLSIETTEKG AAGTFISNGG 360
RIESKGLLVI ETGEDISLRN GAVVQNNGSR PATTVLNAGH NLVIESKTNV NNAKGSANLS 420
AGGRTTINDA TIQAGSSVYS STKGDTELGE NTRIIAENVT VLSNGSIGSA AVIEAKDTAH 480
IESGKPLSLE TSTVASNIRL NNGNIKGGKQ LALLADDNIT AKTTNLNTPG NLYVHTGKDL 540
NLNVDKDLSA ASIHLKSDNA AHITGTSKTL TASKDMGVEA GLLNVTNTNL RTNSGNLHIQ 600
AAKGNIQLRN TKLNAAKALE TTALQGNIVS DGLHAVSADG HVSLLANGNA DFTGHNTLTA 660
KADVNAGSVG KGRLKADNTN ITSSSGDITL VAGNGIQLGD GKQRNSINGK HISIKNNGGN 720
ADLKNLNVHA KSGALNIHSD RALSIENTKL ESTHNTHLNA QHERVTLNQV DAYAHRHLSI 780
TGSQIWQNDK LPSANKLVAN GVLALNARYS QIADNTTLRA GAINLTAGTA LVKRGNINWS 840
TVSTKTLEDN AELKPLAGRL NIEAGSGTLT IEPANRISAH TDLSIKTGGK LLLSAKGGNA 900
GAPSAQVSSL EAKGNIRLVT GETDLRGSKI TAGKNLVVAT TKGKLNIEAV NNSFSNYFPT 960
QKAAELNQKS KELEQQIAQL KKSSPKSKLI PTLQEERDRL AFYIQAINKE VKGKKPKGKE 1020
YLQAKLSAQN IDLISAQGIE ISGSDITASK KLNLHAAGVL PKAADSEAAA ILIDGITDQY 1080
EIGKPTYKSH YDKAALNKPS RLTGRTGVSI HAAAALDDAR IIIGASEIKA PSGSIDIKAH 1140
SDIVLEAGQN DAYTFLKTKG KSGKIIRKTK FTSTRDHLIM PAPVELTANG ITLQAGGNIE 1200
ANTTRFNAPA GKVTLVAGEE LQLLAEEGIH KHELDVQKSR RFIGIKVGKS NYSKNELNET 1260
KLPVRVVAQT AATRSGWDTV LEGTEFKTTL AGADIQAGVG EKARVDAKII LKGIVNRIQS 1320
EEKLETNSTV WQKQAGRGST IETLKLPSFE SPTPPKLSAP GGYIVDIPKG NLKTEIEKLS 1380
KQPEYAYLKQ LQVAKNINWN QVQLAYDRWD YKQEGLTEAG AAIIALAVTV VTSGAGTGAV 1440
LGLNGAAAAA TDAAFASLAS QASVSFINNK GDVGKTLKEL GRSSTVKNLV VAAATAGVAD 1500
KIGASALNNV SDKQWINNLT VNLANAGSAA LINTAINGGS LKDNLGDAAL GAIVSTVHGE 1560
VASKIKFNLS EDYITHKIAH AIAGCAAAAA NKGKCQDGAI GAAVGEIVGE ALTNGKNPAT 1620
LTAKEREQIL AYSKLVAGTV SGVVGGDVNT AANAAKVAIE NNLLSQEEYA LREKLIKKAK 1680
GKGLLSLDWG SLTEQEARQF IYLIEKDRYS NQLLDRYQKN PSSLNNQEKN ILAYFINQTS 1740
GGNTAWAASI LKTPQSMGNL TIPSKDINNT LSKAYQTLSR YDSFDYKSAV AAQPALYLLN 1800
GPLGFSVKAA TVAAGGYNIG QGAKAISNGE YLHGTVQVVN GTLMVAGSVS AQAAISAKPA 1860
PVTRYLSNDS APALRQALTA ESQRIRMKLP EEYRQIGNLA IAKIDVKGLP QRMEAFSSFQ 1920
KGEHGFISLP ETKIFKPISV DKYHNIASPP RGTLRNIDGE YKLLETIAQQ LGNNRNVSGR 1980
IDLFTELKAC QSCSNVILEF RNRYPNIQLN IFTGK 2015
<212> Type : PRT
<211> Length : 2015
SequenceName : SEQ ID 374
SequenceDescription :

Sequence

<213> OrganismName : Neisseria meningitidis Z2491
<400> PreSequenceString :
MDLIQTPNKQ FVDGDRRTPG TPVPAWWLNQ LQGELYSILN AVGIEPNKAD HAQVLSAIKT 60
LAADASQVAS IDALRKYSGT GYVNVNAYHA NTTVGGGVFV ADKADKSTAD NGCTVIVSTD 120
GTRWKRVFSG MLNLHDFGYV ASKNNALSTL NAAESAALDV VVDCLGLSID TGNIYPQKNK 180
YTNGKFVING KTVDVQYQPI RSGIGRFISG TGAAANLKSN EWTGAGLIVI GEGAMEQMEK 240
CVSSIAIGDR AQGFSKVSRD NIAIGADSLI NVQAATEWYD QSRMEGTRNI GIGGNAGRGI 300
TSGYSNVSIG RNAGQGLGEG SSNIALGAGA MAGTAPVGFS GDIEVFWPSS TSRTIAIGEA 360
VLQTYQGRAA QTAIGANAAR NTKKAEKVTA IGSAAMENLE RNRAPNGGDV VWTGTEAGTY 420
AQSGKNITLT FPNIRGAQAT YWVGIRLTSG TAQTLQNDVV PAQVVSVNGN TLIIQSSKEL 480
TATGAAELKY VYSVNSTATK NEELTIIGAN AMNKALTAGY STIIGVDAAL LGDNYQKTTA 540
IGASSLRTGS HISTTAIGYW VIPLASSEKC VAIGDSAGYR NVQGDFLTGK ITNSIAIGYG 600
ARINGDNEIQ IGTTGQTLYA PTAVNIRSDG RDKADVKPLT NGLDFVMKLK PMTGYYDRRD 660
SYVDELFKDL PADERADKVR EWWANPIKDG SHKEDRLRHW FIAQDIAALE DEYGRLPMVN 720
KTNDTYTVEY ETFIPVLTKA IQEMAARIET LETEMKESKK 760
<212> Type : PRT

<211> Length : 760
SequenceName : SEQ ID 375
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MKNISRKCFM TSVVCIILGG ILLGAGYATG GLQDIKHQTA PKKVIKTFDQ ITALDIDSSA 60
STITVETGPV QRPTVTYYTH PKFIDPIVTT LTGKTLSLSQ KPKDIVITGG IEILGFTLNN 120
SRQEKNYRSI TITVPEKTSL NEVKGSNVPH TTLSNLTVQD MQFDGNLTLL HTKVKKATIT 180
GMLEATKSQL TNLELKADYS FSNLTDSSVE NGTISLGNGQ LTTKDTTLKA INIQSLHPGG 240
IEAERTTLEN VTFTVSKSKE EEEENDYYDN DAIFTAHALT LKGTNTISGG DIDVDITLTK 300
AKAIAYRART ENGKVSLGSQ LTPAKIGKES TSDVISYVAE NKAATGNLTV NLNKGDITIK 360

<212> Type : PRT
<211> Length : 360
SequenceName : SEQ ID 376
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MFKKENLKQR YFNFGLVALA LTILAIIFAF SSKNADTKSY AKKSESKMVT IDKAPKNNHA 60
ITKEESKEKA KSIASEPIPT VENSVAPTVT EEAPVVQQEV TQTVQQVSSV AYNPNNVVLS 120
NGNTAGIVGS QAAAQMAAAT GVPQSTWEHI IARESNGNPN AANASGASGL FQTMPGWGST 180
ATVEDQVNAA LKAYSAQGLS AWGY 204
<212> Type : PRT
<211> Length : 204
SequenceName : SEQ ID 377
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MLEELKTLIK NPKLMITMIG VALVPALYNL SFLGSMWDPY GRVNDLPIAV VNHDKPAKRA 60
DKSLTIGNDM VDKMSKSKDL DYHFVSSKSA QKGLKKGDYY MVITLPEDLS QRATTLLNPE 120
PQKLTIRYQT SKGHGMVAAK MGETAMAKLK ESVSQNITKT YTSAVFSSMT DLQSGLKEAS 180
TGSQALDSGA KTAQMGSQML SDNLAGLSSA SWQFQQGTNR LTSGLTAYTA GVSQVKDGLG 240
QLSTDMPVYL NGVSRLSQGA SQLNQGLSQL TQSTTLSDDK AKRIQSLEVG LPVLNQGIQQ 300
LNENLSTMQV PKLNTDELGN NLAAIAQAAQ QLLVKEAAAH KEQLAVLQAT SAYQSLTAEQ 360
QGELTAALTQ TDKGEAVAPA QTILRSVQTL STSLQSLSQE DQSKQLEQLK EAVAQIANQS 420
NQALPGASSA LTELSTGLAK VNGSLNQQVL PGSNQLTTGL AQLNRYNTAI GSGVIKLSEG 480
ANALSSKSGE LLDGSHQLSE GATKLADGSS QLSQGGHQLT SGLTELSTGL SILNGSLAKA 540
SQQLSLVSVT DKNAKAVAKP LVLNEKDKDG VKTNGIGMAP YMIAVSLMVV ALSTNVIFAN 600
SLSGRPVKDK WDWAKQKFVI NGFISTMGSI VLYLAIQLLG FEARYGMETL GFIMLSGWTF 660
MALVTALVGW DDRYGSFASL VMLLLQVGSS GGSYPIELSG AFFQKLHPFL PMTYVVSGLR 720
QTISLSGHIG VEVKVLTGFL LAFMVLSLLI YRPKKTV 757
<212> Type : PRT
<211> Length : 757
SequenceName : SEQ ID 378
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MSRDPTYTIN EHDLSFADGR FYVTFKADKS SETVRLNSSC LGNTIIKKLQ VEDDNTMHDF 60
VKPKVTTQQA FGLAQQVKEL DLQLKDPKSD LWGKIKFNNK AMLVEYANKE MSSAIAQSAE 120
QILLQVKSID DERYSKFEQT LNGIKQTVKS ESVESARTQL ASMFDSRISG LDGKYSRLSQ 180
TIDSLSSRLD DGVGNYSTLS QKVSGIDLRV SNAANDVSRL SQTAQGLQSQ ITNANQNYSS 240
LSQTVQGLQT TVRDNQSNAT SRINQLSDLI STKVSKGDVE TTIAQSYDKI AFAIRDKLPA 300
SKMSGSEIIS AINLDRSGVK ITGKNITLDG NSYISNAVIK DAHIANMDAG KINTGYLNAN 360
RIATEAITGE KIKMDYAFFN KLTANEGYFR TLFAKDIFAT SVQSVTLSAS KITGGVLAAT 420
NGASQWDLNN ANMTFNRDAT INFNSKNNAL VRKDGTHTAF VHFSNATPKG YRGSALYASI 480

GITSSGDGID SASSGRFAGL RSFRYATGYN HTAAVDQTEL YGDNVLIADD FSINRGFKFR 540
PDKMEKVLDM NDLYAAVVAL GRCWGHLANV GWNTAHSNFT SAVSRELNNY ITKI 594

<212> Type : PRT
<211> Length : 594
SequenceName : SEQ ID 379
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MAADGKVTIL VDVDGKQVKV LNSELDKVAK HGDKGSSSLK KFAVGAGVFK LASAAVDLVS 60
QSLGKAITRF DTLEKYPRVM KAMGHSAEDV ARSTDKLANG IDGLPTTLDE VVGTAQRLTS 120
ITKDINKSTN LTLALNNAFL ASGASSEAAS RGLEQYAQML SAGKVDMQAW KTLQETMPYA 180
LQQTAEAFGF AGASAQKDFY EALKNGQITF DQFSNKLIEL NDGVGGFAEL AKENSKGIET 240
SFNNIKNAIA KGVANSIKAL DDLSKAATGK GIADHFDSLK VVINASFSAI NASIKASTPL 300
FKLLFSVIGA GISVVKALSP ALVGVASGLA AMRAVNETIT MIKALNRAWV MASASMSIGA 360
TTIKTVTAVQ AVSTTMTKAD MVARLSQLGV LKASTVIYGV MTGAISLSTA ATIASTAAVT 420
ALKAALVALT GPVGWVVGAI GALVAVGVSL WSWLTKESDE TKKLKKEQEG LVESNKQLRD 480
SVREGVQERK KGLESVKEST AAHQKLADEI IKLAAKENKT AGEKQNLKNK IDQLNGSIDG 540
LNLAYDKNSN SLSHNADQIK SRISAMEAES TWQTAQQNLL NIEQKRSEVS KKLAENADLR 600
KKWNEEANVS DSVRKEKIAE LTEEEAKLKN MQTQLQEEYN KTSATQQAAA DAMAAAEESG 660
SARQVIAYEN MSEAQRTAID NMRTKYSELL ETTTSIFDAI EQKTALSVDQ MNTNLEKNRA 720
ATEQWATNLE ILAQRGVDQG ILEQLRRMGP EGATQTQVFV DATDAELAPL QENFRAATET 780
AKNAMGSVLD SAGVEMPEKV KGMVTNVSTG LQAELQAANF AQLGQEIPNG VSQGISQGAG 840
KASDASVKMG QEVKRSFQGE LGIHSPSRVF TEYGGHITDG LSNGVTNGTS KVMQTMQSLA 900
QQMSQKGQQI VNDMRSKSNQ ITDAFSTMSG PMHSHGVNAM QGLANGIYAG SGAALAAAQS 960
IAARITATIQ SALDIHSPSR VMRDEVGRFI PQGIAVGIDA DRKVIDSSMQ KLKESMTINA 1020
TPEIASGFGG GVAGIANQTT NNSNNSFTLN VKVDESDGNS HEKYQRLFRE FSWYIQQQQG 1080
RLGDVK 1086
<212> Type : PRT
<211> Length : 1086
SequenceName : SEQ ID 380
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MAKEPWEEKI VDDTIGTRTR KSRNAFISTP WLTALLSVFF VIIVAILFIF FYTSNSGSNR 60
QAETNGFYGA STHKKTRKAS NAKKTSSSST TTDTTPSSEE TLASSEGTGE TLTVLAGEGA 120
ASIAARAGIS VEQLQALNPE HMTQGYWYAN PGDQVTIK 158
<212> Type : PRT
<211> Length : 158
SequenceName : SEQ ID 381
SequenceDescription :

Sequence

<213> OrganismName : Streptococcus pyogenes MGAS8232
<400> PreSequenceString :
MSKRGKIKIT TKTKLITASV ITLVLIITGV VLWKQQQNTL TADIAKEPYS TVSVTEGSIA 60
SSTLLSGTVK ALSEEYIYFD ANKGNDATVT VKIGDQVTQG QQLVQYNTTT AQSAYDTAVR 120
SLNKIGRQIN HLKTYGVPAV STETNKDEAT GEETTTTVQP SAQQNANYKQ QLQDLNDAYA 180
DAQAEVNKAQ IALNDTVVIS SVSGTVVEVN NDIDPSSKNS QTLVHVATEG QLQVKGTLTE 240
YDLANVKVGQ SVKIKSKVYS NQEWTGKISY VSNYPTESNA GSTTPAGSTG AGSSTGAAYD 300
YKIDIISPLN QLKQGFTVSV EVVNEAKQAL VPLTAVIKKD KKHYVWTYDD ATGKAKKVEV 360
TLGNADAQQQ EIHKGVAVGD IVIANPDKNI KPDKKLEGVI SIGTNTKPEK DSQSKNKKSG 420
VDK 423
<212> Type : PRT
<211> Length : 423
SequenceName : SEQ ID 382
SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum
<400> PreSequenceString :
MLRLPTARAC ITMGTMIRHT FTHRCGALLC ALALGSSTMA ATAAAKPKKG QMQKLRQRPV 60
WAPTGGRYAS LDGAFTALAN DASFFEANPA GSANMTHGEL AFFHTTGFGS FHAETLSYVG 120
QSGNWGYGAS MRMFFPESGF DFSTTTEPVC TPASNPIKQR GAIGIINFAR RIGGLSLGAN 180
LKAGFRDAQG LQHTSVSSDI GLQWVGNVAK SFTSEEPNLY IGLAATNLGL TVKVSDKIEN 240
CTSTCEKCGC CKERCCCNGK KACCKDCDCN CPCQDCNDKG TVHATDTMLR AGFAYRPFSW 300
FLFSLGATTS MNVQTLASSD AKSLYQNLAY SIGAMFDPFS FLSLSSSFRI NHKANMRVGV 360
GAEARIARIK LNAGYRCDVS DISSGSGCTG AKASHYLSLG GAILLGRN 408
<212> Type : PRT
<211> Length : 408
SequenceName : SEQ ID 383
SequenceDescription :

Sequence

<213> OrganismName : Treponema pallidum
<400> PreSequenceString :
MSRTFRAWQC VGALCALSPL LPAYSSEGVR EVPPSQSPQV VVAYEPIRPG DQLLKIGIVA 60
GCQLYIAGGN GTNGSSSSGT NGNGNGKLLG GGGFHLGYEY FFTKNFSLGG QVSFECYRTT 120
GSNYYFSVPI TVNPTYTFAV GRWRIPLSLG VGLNIQSYLS KKAPGLIAEA SAGLYYQYTP 180
DWSIGGIVAY TQLGDIASSP DKCRAVGLAT IDFGVRYHF 219
<212> Type : PRT
<211> Length : 219
SequenceName : SEQ ID 384
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
atgataaatt taagtaagga agcaacggtg gggaaagcat taacccctat tgctatactt 60
atgatgttgt cttttcctgt agcttctcaa gcggcgggat tagtcataaa aaatggaacg 120
gtatataacg ccaatggtgt gccagtcgtt gacatcaaca aacctaacgg tagcggttta 180
tctcataata tctgggataa cctaaacgtt gataaaaatg gtgtcgtttt caataatagc 240
gctaatgaat ccagtacttc acttgccgga aatattcagg gaaacagtaa tctgacctcc 300
gggtcggcga aggtgatcct gaatgaggtt acttccaaaa atccttcaac cattaatggg 360
atgatggaag ttgcagggga taaagcggat ctgattattg ccaacccgaa tggtattact 420
gtaaacggtg gcggttcaat caatacaggt aaacttacct taaccaccgg gacgccggat 480
atccaggatg acaagctggc cggttactcc gtgaacggcg gtaccattac gctcggtaaa 540
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tctgccgatg agctgaacgt tgttgctggc aataactatg ttaatgccgc aggccaggtg 660
accggtagcg tatccgccac ggggtcccgt aacggttaca gcgtagatgt tgccaaactg 720
ggcggaatgt atgcgaacaa aatcagtctg gtcagcaccg agaaaggtgt gggggttcgc 780
aacctcggcg ttattgctgg ggtgttaat ggtgtcagca tcgattccaa aggtaacctg 840
ttaaacagta acgcccagat tcagtctgca agcacgatca acctgacaac aaatggtact 900
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accggcagtt ctgactctct gggcattatt gcagataccg gcgtagaaat tggtgcgaac 1440
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tacggctgga tcagcggtaa aggcgatgtt gatgtcacgg tgaataacgg caacctgtat 2280
aaccgcaata ccattgcggc tgaaaagggg ctggatattg ccgcgttgaa cggtattgaa 2340
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aacaactcca acagcaatat ggtggggcag aatattgtta ttaacgcggt taacgatatc 2460
aacaaccgtg gcaacattgt cagtgacgct gacctgaacg tgacgaccaa aggcaacctg 2520
tataactatc tctatatggt agggtatggg gatatcgcat tgtcggcaaa tagcgtggcg 2580
aacaataacg cgaccatcga agcgacaggc gatctgatta tcgattcgaa gggtaacgtg 2640
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gcggcaggga cgttctacaa caactatgcc accacgtaca gcgccggtaa tctcgacgtt 3240
tatgcggcgt cgttgaacaa cgccagcgat ggtcgcctgg aagacaatac cgccacgggc 3300
gtgattgcgt ctgacaaaaa cctggatctg agcgttgata acagtgtcac taactatggt 3360
tggatcagcg gtaaaggaga tgtgcatttc aatgttctga aaggcacgct gtataaccgt 3420
aatgccatcg cggcggacaa cgcgctgacc attaatgccc tgaacggtgt tgagaacttt 3480
aaagacattg tggcgggtac tgcgctgact attgatacgc agaagtatgt taccaacaac 3540
agcaacagta atatgttggg acaaaccatc gcgatcaatg ccgtgaatga cattaataac 3600
cgtggaaata ttgtgggtga ttattctctg ggtgttaaaa ccaccggtaa tatttataac 3660
tacctcaata tgctgagtta tggtgtcgct ggcgtatcgg caaataaggt tacgaatagc 3720
ggtaaagacg ctgttctcgg tggcttctac ggtttagcgt tagaagcaaa cgaaactgat 3780
aacaccggta ctattgtcgg catgtaa 3807

<212> Type : DNA
<211> Length : 3807
SequenceName : SEQ ID 385
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

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gctgatgttg cagcaaagct aaggtcgctt aaacgctact cagtattcac ttttcagagg 120
atgaaattta tgaacaggac cagtccctat tattgtcgtc gctcagtact ttccttattg 180
atatctgcct tgatatatgc cccgcccggg atggctgcct tcactcctga tgttattggt 240
gtggtaaacg atgagactgt agatggcagc caacgagtag atgaacgagg tacaacaaat 300
aacactcata ttatcaacca tggccagcag aatgtttatg gcggggtatc taatggaagt 360
cttattgaat ctggtggata tcaagatgta ggaaggcata acaattatgt ggggcagtct 420
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acgataatcg agagtggcaa tcaggacgtt tataaagggg gtatcagcaa tggaacgaca 540
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<212> Type : DNA
<211> Length : 4716
SequenceName : SEQ ID 386
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 2916
SequenceName : SEQ ID 387
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

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gtttatgtaa accttgcgcc tgccgtgaat gtggggcaaa acctggtcgt agatctttcg    180
acgcaaatct tttgccataa cgattatccg gaaaccatta cagactatgt cacactgcaa    240
cgaggctcgg cttatggcgg cgtgttatct aatttttccg ggaccgtaaa atatagtggc    300
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gataagccgt ggccggtggc gctttatttg acgcctgtga gcagtgcggg cggggtggcg    420
attaaagctg gctcattaat tgccgtgctt atttgcgac agaccaaaaa ctataacagc     480
gatgatttcc agtttgtgtg gaatatttac gccaataatg atgtggtagt gcctactggc    540
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<212> Type : DNA

<211> Length : 903
SequenceName : SEQ ID 388
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

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cccacaattg ctgccagcga tttaatgcaa cgtggtcagt cagatcgcgt accgttagtt    240
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gttgggattg gcattgaaac tgccggaggg gcggctgtac ctattaacag taccacaggt    420
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<212> Type : DNA
<211> Length : 549
SequenceName : SEQ ID 389
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

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gaaaccgtga acgatggaac actgacaaat catgacaacc agattgtctt cggtacggcc    240
aacggaatga ccatcagtac cggcctggaa ctggggccgg acagtgaaga aaacaccggt    300
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caggtcgtgc tggagggggg aacagccagt gatacggtta ttcgtgacgg cgggggacag    420
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<212> Type : DNA
<211> Length : 2850
      SequenceName : SEQ ID 390
      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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tttcctctga caacggtcag tgcagcaaac aatgtgcctg gaaatacatt aatagatatt     180
gctaatgcaa catcttctga aaattatagc gttctgtgta actgtgattc aaaacatagc     240
aatggcgctt atcacgaaat atattatacc gcagaccctg ctcccggtat ggtttatagc     300
accaccgcaa gtggtcttgc tttttactat cttaacgaat atgtcgatgt gggaacaaaa     360
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<212> Type : DNA
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      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
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<212> Type : DNA
<211> Length : 4254
SequenceName : SEQ ID 392
SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

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<212> Type : DNA
<211> Length : 4740
SequenceName : SEQ ID 393
SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
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<211> Length : 2805
SequenceName : SEQ ID 394
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 1071
SequenceName : SEQ ID 396
SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
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<211> Length : 549
SequenceName : SEQ ID 398
SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
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<212> Type : DNA
<211> Length : 564
SequenceName : SEQ ID 399
SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
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<212> Type : DNA
<211> Length : 3753
SequenceName : SEQ ID 400
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :

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<213> OrganismName : Escherichia coli O157:H7
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<212> Type : DNA
<211> Length : 564
SequenceName : SEQ ID 402
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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ggcggcaacg gtgcagcggt tgaccagact gcatctaatt ccaccgtcaa cgtaactcag 420
gttggctttg gtaacaacgc gaccgctcat cagtactaa 459
<212> Type : DNA
<211> Length : 459
SequenceName : SEQ ID 403
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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ccattacctt cacaaaccga cggtgcaggg gggcgtggtc agctcattaa ctctacgggg 120

ccgttgggat ctcgtgcgct atttacgcct gtaaggaatt ctatggctga ttctggcgac 180
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<212> Type : DNA
<211> Length : 1677
SequenceName : SEQ ID 404
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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atcaacggtc aaaccaattc agtagtattg atgccgaccg tagccatggc tgacttcggt 180
gcaactttag ctgatggtca gagcgcaggc cagacgccgt ttacggtttc tgtgtctaac 240
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gacgctagca cgggtgttat gggaaaccgt gataccagca gcgatgcggc gaaaggcttt 360
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<212> Type : DNA
<211> Length : 561
SequenceName : SEQ ID 405
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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atgaacgtga aaggcgatac ccaagggaac actcgcgttc gggttgataa cattggcggc 180
gtcggtgcgc aaacggtcaa cggtattgaa ctcattgagg ttggcggtaa ttctgcaggt 240
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cgaaatctcg gtgaagtacg taccggggtt gaggcgaaag taaataacaa ccttagcctg   1320
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<212> Type : DNA
<211> Length : 1401
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      SequenceDescription :

Sequence
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cctttgtcat ctgccgaact ctattttaat ccgcgctttt tagcggatga tccccaggct    180
gtggccgatt tatcgcgttt tgaaaatggg caagaattac cgccagggac gtatcgcgtc    240
gatatctatt tgaataatgg ttatatggca acgcgtgatg tcacatttaa tacgggcgac    300
agtgaacaag ggattgttcc ctgcctgaca cgcgcgcaac tcgccagtat ggggctgaat    360
acggcttctg tcgccggtat gaatctgctg gcggatgatg cctgtgtgcc attaaccaca    420
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aataaatggc agcatatcaa tacctggctt gagcgagaca taataccgtt acgttcccgg    780
ctgacgctgg gtgatggtta tactcagggt gatattttcg atggtattaa ctttcgcggc    840
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ggaaaagttc aggtgaaatg gggagaagag gaaaatgctc attgtgtcgc caattatcaa   2580
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<212> Type : DNA
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<211> Length : 2637
SequenceName : SEQ ID 407
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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aatccgtata ttggcgtcaa ttttggcgtt aaaaccctgg aggaagaaga aaatacgact 180
ggggtagtaa aagacaaatt ttatcagtgg aacgaatcga atgattatta tgtttcctgt 240
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gaccccagct atccccaggc gattaagacg tcacgtcctg gcgtgggcgt ggtggtgacc 900
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gatgcagaca gtatcgcgtg a 981
<212> Type : DNA
<211> Length : 981
SequenceName : SEQ ID 408
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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tatcaataa 549
<212> Type : DNA
<211> Length : 549
SequenceName : SEQ ID 409
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 606
SequenceName : SEQ ID 410

SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 2511
SequenceName : SEQ ID 411
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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acagaaatag ccgaagctac atgggatgta aatattcaac taagaggcga tgccataggg 240
tgtaaatctc ttggggatag taaggcagtt cactttctta atacagctga cccaagttta 300
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ctacctgcac aaagtggcgc agataacttc ataccaagca cccagacgaa atgggcctat 480
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<212> Type : DNA
<211> Length : 1110
      SequenceName : SEQ ID 412
      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
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tttttaatgg gaactggcgc atcaacgatt gatgttaaac gttatgctca aggcaacccg     180
acaccgccgg gtctctataa tgtccgcgta tttgtaaacg gtcaggcgac ttccagctta     240
gaaattccgt ttgtggatat tggcgaaaac agtgcggcgg cctgtcttac ccataaaaac     300
ctggcgcaac ttcacattaa gcaacctgaa cagcctgtca ctttactcgc cagagaaggt     360
gaagaagagg attgtctgga tctggcaaag tcatacgaaa aggcggatgt gtgctttgac     420
ggtagtgacc agtttctcga tctgacgatc cctcaggcct atgttctgaa aagctatggc     480
ggctacgttg acccttcttt atgggaatcg ggaattaacg ctgccacact ggcatatacc     540
ctgaacgcgt atcacacaag ttcagataac gacaatagtg acagcgtcta tggcgcgttc     600
aactcaggta tcaatttagg agcctggcac tttcgtgcgc gcggtaacta taactggaca     660
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ccttccggct ttggtagcga actggtcgtg accattgaag aagcggatgg ttccaaacgc    1020
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agcggctccg ttgttttgac ccgtttcgaa actgacgagg ggcgttctgc cgtgctgaat    2340
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<212> Type : DNA
<211> Length : 2601
      SequenceName : SEQ ID 413
      SequenceDescription :
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Sequence
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<213> OrganismName : Escherichia coli O157:H7
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actaaagctt gcgagatgga aaaaagcgat ctcgaagtcg atatgggaac aatgacgctg     180
caaaaacctg cggcagtcgg tacggtgttg agcaagaaag atttcaccat tgaactcaaa     240
gagtgcgatg ggatatccaa agcgaccgtt gagatggaca gtcagtcgga cagcgatgat     300
gattccatgt ttgcccttga ggctggtggc gcaacgggtg ttgcgttgaa gatagaggac     360
gataaaggaa cgcagcaagt tcccaaaggc tccagcggaa cgccgattga atgggcgatt     420
gatggcgaaa ccacgtcgct tcactaccag gcgagttatg tggtcgtcaa cactcaggcc     480
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<212> Type : DNA
<211> Length : 531
      SequenceName : SEQ ID 414
      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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tcatcggatt cgcttaattt taccgtagat ctccaaaaaa acagtgccag acaatttcca     180
acgaccggta gcacaagtcc agccgtccct tttcagatta cgttaagtga atgcagcaaa     240
gggacaacgg gggttcgggt tgcatttaac ggtattgagg acgcagaaaa taatactctg     300
ttgaaactgg atgagggaag caatacggcc tccggtttag gtatagaaat actggacgga     360
aatatgcgtc cggtgaaact gaatgacctt catgccggga tgcagtggat cccactggta     420
ccagaacaga acaatatttt gccttactcc gctcgtctga agtcaactca gaagtccgtc     480
aatccgggac tggtgagggc ttcggcaacc tttacccttg aatttcaata a              531

<212> Type : DNA
<211> Length : 531
      SequenceName : SEQ ID 415
      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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gtttccacca ccaatgccac ggttgatctc ggcgatcttt attctttcag tctgatgtct     180
gccggggcgg catcggcctg gcatgatgtt gcgcttgagt tgactaattg tccggtggga     240
acgtcaaggg tcactgccag cttcagcggg gcagccgaca gtaccggata ttataaaaac     300
caggggaccg cgcaaaacat ccagttagag ctacaggatg acagtggcaa cacattgaat     360
actggcgcaa ccaaaacagt tcaggtggat gattcctcac aatcagcgca cttcccgtta     420
caggtcagag cattgacggt aaatggcgga gccactcagg gaaccattca ggcagtgatt     480
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<212> Type : DNA
<211> Length : 504
      SequenceName : SEQ ID 416
      SequenceDescription :

Sequence
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<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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gatgatgtta cggtgaacca gacagataac gtgacaggac gggagtttac ctctgcaacg     180
ctaagtagca ctaactggca atacgcctgt tcctgctctg cgggtaaggc agttaaactt     240
gtctatatgg tcagccccgt acttaccacc actggacatc agacaggata ttacaaactc     300
aatgacagcc tggatattaa aaccatgaac cgccccggaa atcctggaga ctaa           354
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<212> Type : DNA
<211> Length : 354
SequenceName : SEQ ID 417
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400>·PreSequenceString :
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gtagatactg gtatgcatag cgttaccact gatggcgtgg ttaccctgga tactgcgaat 180
gttactgata cttttgctga agttagcgca actgctgtcg gtttactgcc gaaagagttc 240
atgatttctg ttgagtgtga tccaggtgct ccgaagaatg ctgagttaac tatgggttct 300
gcaagttacg cgaacaccag cggtaccctg aataacaata tgaacatcac tgttaacggt 360
attgcaccgg ctcagaacgt aaacattgca gttcataaca tgaaaaacaa agctggcgct 420
gctgaaatta agcaggtcca tatgaacaac tcttctgaag ttcaggaact gacattagac 480
gcagaaggta aaggccagta cgtatttaac gcatcttacg ttaaagcacc gaacagcccg 540
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<212> Type : DNA
<211> Length : 597
SequenceName : SEQ ID 418
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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ctacaggcgg ctgatggaac agtccatttc cgtggtgaaa ttattgacag tacttgcgaa 120
gtcactcctg aaactaaaga tcaggtcgtt gatttaggca aagtaaaccg tacagccttt 180
agtggcgtcg atgatgtggc tgccccgacg gctttttcta tcgatctgac tcaatgcccg 240
gaaaccttta agtccgccgc aattcgtttc gatggtaatg aagatgctca tggtaatggc 300
aacctggcaa ttggtacccc gctggataac tctaacgatg ctgccgctgg tattagcccg 360
agtgataaca gtggggatta tactggtgcg ggtgccgtta gtgcagcgaa aggcgtagct 420
attcgtttat ataaccgtgc agataacact caggtcaagt tatatgaaaa ttctgcatca 480
actccgattt ctaatggtaa tgcatccatg aagttcatgg ctcgttatat tgctacggaa 540
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taa 603
<212> Type : DNA
<211> Length : 603
SequenceName : SEQ ID 419
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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gccgggaatt atgacagcgc ctcgccgcgt ttcgggcagc ttgatctgat ctacggttta 120
ccgtggggga tgacggccta cggcggcgta ttaatctcta ataattacaa tgcatttaca 180
ttagggatag ggaaaaactt tggttatatc ggggcgattt ccattgatgt gacgcaggct 240
aaaagcgaac tgaataacga tcgcgatagc cagggacaat cttatcgttt cttatattcc 300
aagagcttcg aaagcggcac cgatttccgc cttgcgggct atcggtactc taccagcggt 360
ttctatacct tccaggaagc caccgatgtg cgcagtgacg ctgacagcga ctataaccgt 420
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attagcggaa tgccagagga aggacgggta ttgattaaat ggggtaatga cgcgtcgcag 1380
caatgcgtgg cgccttataa attatccctg gaattaaaac agggcggaat tattcctgtt 1440
tcggccaatt gccagtaa 1458
<212> Type : DNA
<211> Length : 1458
SequenceName : SEQ ID 420
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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cgcagcgacc agcaaatatc atttggatta aatgtgccgt ttggtgatat tacgacttcg 240
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acgcttaatg ttcccttcag tcattggatg cgtacagaca gtcagtcggc atttcgtaat 360
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cacggagaga ataaaaatgg cagcattgtc gcggaaaacg gtcaggttta tctgactgga 1020
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tgtcgctaa 1149
<212> Type : DNA
<211> Length : 1149
SequenceName : SEQ ID 421
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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gtgcagtttc cgtccggtaa gggctttaag ttcctggcgg aagtgcgtca gcacacctgg 360
tcatccggta ccaacggcgt ggtggctgca acgttttcac ttcgcctgaa gggtaaaccg 420
gtgtcctatg tggtaccgct ggcgtttgtg aaaaatctgg ataagacact taccgtgaat 480
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gcctggaaga aggatggtca gccggtagag ggacagacta ctgacacttt cagtaagcca 600
ggtgcgcagt caggtgataa gggggcttat acctgcgagg taacggattc tgcagaacag 660
ccgcagagca ttacctctga tgcgtgtaca gtaacggtta atggtgcggg cggataa 717

<212> Type : DNA
<211> Length : 717
SequenceName : SEQ ID 422
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7

<400> PreSequenceString :
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gccgctgaat caaccaattt tactgttgat ctgatggaaa acgcggcgaa gcaatttaac 180
aacattggcg cgacgactcc tgtcgttcca tttcgtattt tgctgtcacc ctgtggtaac 240
gccgtttctg ccgtaaaagt tgggtttacc ggcgttgcag atagccacaa tgccaacctg 300
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ccgggtaaac caaatacgtt gaatttttac gcccggctaa tggcgacaca ggtgcctgtc 480
actgcggggc atatcaatgc cacggctacc ttcactcttg aatatcagta a 531

<212> Type : DNA
<211> Length : 531
SequenceName : SEQ ID 423
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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atggggagcg aaatctcacc cgcaacaccg tcagatgaag acaactacac ctttgacccg 120
caactcttcc gcggcagcag atttagtcag tcgtcattag caaaactgac aacacgtgag 180
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<212> Type : DNA
<211> Length : 2523
SequenceName : SEQ ID 424
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 2031
SequenceName : SEQ ID 425
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
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<212> Type : DNA
<211> Length : 2517
SequenceName : SEQ ID 426
SequenceDescription :

Sequence

<213> OrganismName : Escherichia coli O157:H7
<400> PreSequenceString :
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<212> Type : DNA
<211> Length : 1035
SequenceName : SEQ ID 427
SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
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atgggcggtg tgagcttgtg ggatcttgcg gttgcgtatc cggtcacctc tcacctgaca   1740
gttcgtggta aaatagccaa cctgttcgac aaagattatg agacagtcta tggctaccaa   1800
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<212> Type : DNA
<211> Length : 1845
      SequenceName : SEQ ID 428
      SequenceDescription :

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<213> OrganismName : Escherichia coli O157:H7
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aagattgacc agacaggaga ttataacctt gcatatattg atcaggcggg cagtgccaat    300
gatgccagta tttcgcaagg tgcttatggt aatactgcga tgattatcca gaaaggttct    360
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<212> Type : DNA
<211> Length : 456
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tggacactac cctctggcat cagtgtcgct cccggtgcgc agatccattt agtgaccgtc    660
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<212> Type : DNA
<211> Length : 702
      SequenceName : SEQ ID 430
      SequenceDescription :
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